```
GAATTCGGAG GAATTATTCA AAACATAAAC ACAATAAACA ATTTGAGTAG TTGCCGCACA    60

CACACACACA CACAGCCCGT GGATTATTAC ACTAAAAGCG ACACTCAATC CAAAAAATCA   120

GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA      171
                       Met His Trp Ile Lys Cys Leu Leu Thr Ala
                         1               5                  10

TTC ATT TGC TTC ACA GTC ATC GTG CAG GTT CAC AGT TCC GGC AGC TTT      219
Phe Ile Cys Phe Thr Val Ile Val Gln Val His Ser Ser Gly Ser Phe
                    15                  20                  25

GAG TTG CGC CTG AAG TAC TTC AGC AAC GAT CAC GGG CGG GAC AAC GAG      267
Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asp His Gly Arg Asp Asn Glu
                30                  35                  40

GGT CGC TGC TGC AGC GGG GAG TCG GAC GGA GCG ACG GGC AAG TGC CTG      315
Gly Arg Cys Cys Ser Gly Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu
            45                  50                  55

GGC AGC TGC AAG ACG CGG TTT CGC GTC TGC CTA AAG CAC TAC CAG GCC      363
Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Gln Ala
        60                  65                  70

ACC ATC GAC ACC ACC TCC CAG TGC ACC TAC GGG GAC GTG ATC ACG CCC      411
Thr Ile Asp Thr Thr Ser Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro
    75                  80                  85                  90

ATT CTC GGC GAG AAC TCG GTC AAT CTG ACC GAC GCC CAG CGC TTC CAG      459
Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asp Ala Gln Arg Phe Gln
                95                  100                 105

AAC AAG GGC TTC ACG AAT CCC ATC CAG TTC CCC TTC TCG TTC TCA TGG      507
Asn Lys Gly Phe Thr Asn Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp
            110                 115                 120
```

FIG.1A

```
CCG GGT ACC TTC TCG CTG ATC GTC GAG GCC TGG CAT GAT ACG AAC AAT    555
Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asp Thr Asn Asn
        125                 130                 135

AGC GGC AAT GCG CGA ACC AAC AAG CTC CTC ATC CAG CGA CTC TTG GTG    603
Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Gln Arg Leu Leu Val
    140                 145                 150

CAG CAG GTA CTG GAG GTG TCC TCC GAA TGG AAG ACG AAC AAG TCG GAA    651
Gln Gln Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu
155                 160                 165                 170

TCG CAG TAC ACG TCG CTG GAG TAC GAT TTC CGT GTC ACC TGC GAT CTC    699
Ser Gln Tyr Thr Ser Leu Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu
                175                 180                 185

AAC TAC TAC GGA TCC GGC TGT GCC AAG TTC TGC CGG CCC CGC GAC GAT    747
Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp
            190                 195                 200

TCA TTT GGA CAC TCG ACT TGC TCG GAG ACG GGC GAA ATT ATC TGT TTG    795
Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu
        205                 210                 215

ACC GGA TGG CAG GGC GAT TAC TGT CAC ATA CCC AAA TGC GCC AAA GGC    843
Thr Gly Trp Gln Gly Asp Tyr Cys His Ile Pro Lys Cys Ala Lys Gly
    220                 225                 230

TGT GAA CAT GGA CAT TGC GAC AAA CCC AAT CAA TGC GTT TGC CAA CTG    891
Cys Glu His Gly His Cys Asp Lys Pro Asn Gln Cys Val Cys Gln Leu
235                 240                 245                 250

GGC TGG AAG GGA GCC TTG TGC AAC GAG TGC GTT CTG GAA CCG AAC TGC    939
Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys
                255                 260                 265
```

FIG. 1B

```
ATC CAT GGC ACC TGC AAC AAA CCC TGG ACT TGC ATC TGC AAC GAG GGT      987
Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly
            270                 275                 280

TGG GGA GGC TTG TAC TGC AAC CAG GAT CTG AAC TAC TGC ACC AAC CAC     1035
Trp Gly Gly Leu Tyr Cys Asn Gln Asp Leu Asn Tyr Cys Thr Asn His
        285                 290                 295

AGA CCC TGC AAG AAT GGC GGA ACC TGC TTC AAC ACC GGC GAG GGA TTG     1083
Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu
    300                 305                 310

TAC ACA TGC AAA TGC GCT CCA GGA TAC AGT GGT GAT GAT TGC GAA AAT     1131
Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn
315                 320                 325                 330

GAG ATC TAC TCC TGC GAT GCC GAT GTC AAT CCC TGC CAG AAT GGT GGT     1179
Glu Ile Tyr Ser Cys Asp Ala Asp Val Asn Pro Cys Gln Asn Gly Gly
                335                 340                 345

ACC TGC ATC GAT GAG CCG CAC ACA AAA ACC GGC TAC AAG TGT CAT TGC     1227
Thr Cys Ile Asp Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys
            350                 355                 360

GCC AAC GGC TGG AGC GGA AAG ATG TGC GAG GAG AAA GTG CTC ACG TGT     1275
Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys
        365                 370                 375

TCG GAC AAA CCC TGT CAT CAG GGA ATC TGC CGC AAC GTT CGT CCT GGC     1323
Ser Asp Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly
    380                 385                 390

TTG GGA AGC AAG GGT CAG GGC TAC CAG TGC GAA TGT CCC ATT GGC TAC     1371
Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr
395                 400                 405                 410
```

FIG.1C

```
AGC GGA CCC AAC TGC GAT CTC CAG CTG GAC AAC TGC AGT CCG AAT CCA     1419
Ser Gly Pro Asn Cys Asp Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro
                415                 420                 425

TGC ATA AAC GGT GGA AGC TGT CAG CCG AGC GGA AAG TGT ATT TGC CCA     1467
Cys Ile Asn Gly Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro
            430                 435                 440

GCG GGA TTT TCG GGA ACG AGA TGC GAG ACC AAC ATT GAC GAT TGT CTT     1515
Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu
        445                 450                 455

GGC CAC CAG TGC GAG AAC GGA GGC ACC TGC ATA GAT ATG GTC AAC CAA     1563
Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asp Met Val Asn Gln
    460                 465                 470

TAT CGC TGC CAA TGC GTT CCC GGT TTC CAT GGC ACC CAC TGT AGT AGC     1611
Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser
475                 480                 485                 490

AAA GTT GAC TTG TGC CTC ATC AGA CCG TGT GCC AAT GGA GGA ACC TGC     1659
Lys Val Asp Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys
                495                 500                 505

TTG AAT CTC AAC AAC GAT TAC CAG TGC ACC TGT CGT GCG GGA TTT ACT     1707
Leu Asn Leu Asn Asn Asp Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr
            510                 515                 520

GGC AAG GAT TGC TCT GTG GAC ATC GAT GAG TGC AGC AGT GGA CCC TGT     1755
Gly Lys Asp Cys Ser Val Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys
        525                 530                 535

CAT AAC GGC GGC ACT TGC ATG AAC CGC GTC AAT TCG TTC GAA TGC GTG     1803
His Asn Gly Gly Thr Cys Met Asn Arg Val Asn Ser Phe Glu Cys Val
    540                 545                 550
```

FIG. 1D

```
TGT GCC AAT GGT TTC AGG GGC AAG CAG TGC GAT GAG GAG TCC TAC GAT     1851
Cys Ala Asn Gly Phe Arg Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp
555                 560                 565                 570

TCG GTG ACC TTC GAT GCC CAC CAA TAT GGA GCG ACC ACA CAA GCG AGA     1899
Ser Val Thr Phe Asp Ala His Gln Tyr Gly Ala Thr Thr Gln Ala Arg
                    575                 580                 585

GCC GAT GGT TTG ACC AAT GCC CAG GTA GTC CTA ATT GCT GTT TTC TCC     1947
Ala Asp Gly Leu Thr Asn Ala Gln Val Val Leu Ile Ala Val Phe Ser
                590                 595                 600

GTT GCG ATG CCT TTG GTG GCG GTT ATT GCG GCG TGC GTG GTC TTC TGC     1995
Val Ala Met Pro Leu Val Ala Val Ile Ala Ala Cys Val Val Phe Cys
        605                 610                 615

ATG AAG CGC AAG CGT AAG CGT GCT CAG GAA AAG GAC GAC GCG GAG GCC     2043
Met Lys Arg Lys Arg Lys Arg Ala Gln Glu Lys Asp Asp Ala Glu Ala
    620                 625                 630

AGG AAG CAG AAC GAA CAG AAT GCG GTG GCC ACA ATG CAT CAC AAT GGC     2091
Arg Lys Gln Asn Glu Gln Asn Ala Val Ala Thr Met His His Asn Gly
635                 640                 645                 650

AGT GGG GTG GGT GTA GCT TTG GCT TCA GCC TCT CTG GGC GGC AAA ACT     2139
Ser Gly Val Gly Val Ala Leu Ala Ser Ala Ser Leu Gly Gly Lys Thr
                655                 660                 665

GGC AGC AAC AGC GGT CTC ACC TTC GAT GGC GGC AAC CCG AAT ATC ATC     2187
Gly Ser Asn Ser Gly Leu Thr Phe Asp Gly Gly Asn Pro Asn Ile Ile
            670                 675                 680

AAA AAC ACC TGG GAC AAG TCG GTC AAC AAC ATT TGT GCC TCA GCA GCA     2235
Lys Asn Thr Trp Asp Lys Ser Val Asn Asn Ile Cys Ala Ser Ala Ala
        685                 690                 695
```

FIG. 1E

```
GCA GCG GCG GCG GCG GCA GCA GCG GCG GAC GAG TGT CTC ATG TAC GGC     2283
Ala Ala Ala Ala Ala Ala Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly
    700                 705                 710

GGA TAT GTG GCC TCG GTG GCG GAT AAC AAC AAT GCC AAC TCA GAC TTT     2331
Gly Tyr Val Ala Ser Val Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe
715                 720                 725                 730

TGT GTG GCT CCG CTA CAA AGA GCC AAG TCG CAA AAG CAA CTC AAC ACC     2379
Cys Val Ala Pro Leu Gln Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr
                735                 740                 745

GAT CCC ACG CTC ATG CAC CGC GGT TCG CCG GCA GGC AGC TCA GCC AAG     2427
Asp Pro Thr Leu Met His Arg Gly Ser Pro Ala Gly Ser Ser Ala Lys
            750                 755                 760

GGA GCG TCT GGC GGA GGA CCG GGA GCG GCG GAG GGC AAG AGG ATC TCT     2475
Gly Ala Ser Gly Gly Gly Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser
        765                 770                 775

GTT TTA GGC GAG GGT TCC TAC TGT AGC CAG CGT TGG CCC TCG TTG GCG     2523
Val Leu Gly Glu Gly Ser Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala
    780                 785                 790

GCG GCG GGA GTG GCC GGA GCC TGT TCA TCC CAG CTA ATG GCT GCA GCT     2571
Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Gln Leu Met Ala Ala Ala
795                 800                 805                 810

TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG CGA TCC GTG     2619
Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val
                815                 820                 825

GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT        2670
Val Cys Gly Thr Pro His Met
            830

AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGGTT   2730
GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTTGTTG ATTGAAGCAG TTTAGTCGTC   2790
ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG   2850
TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC                      2892
```

FIG. 1F

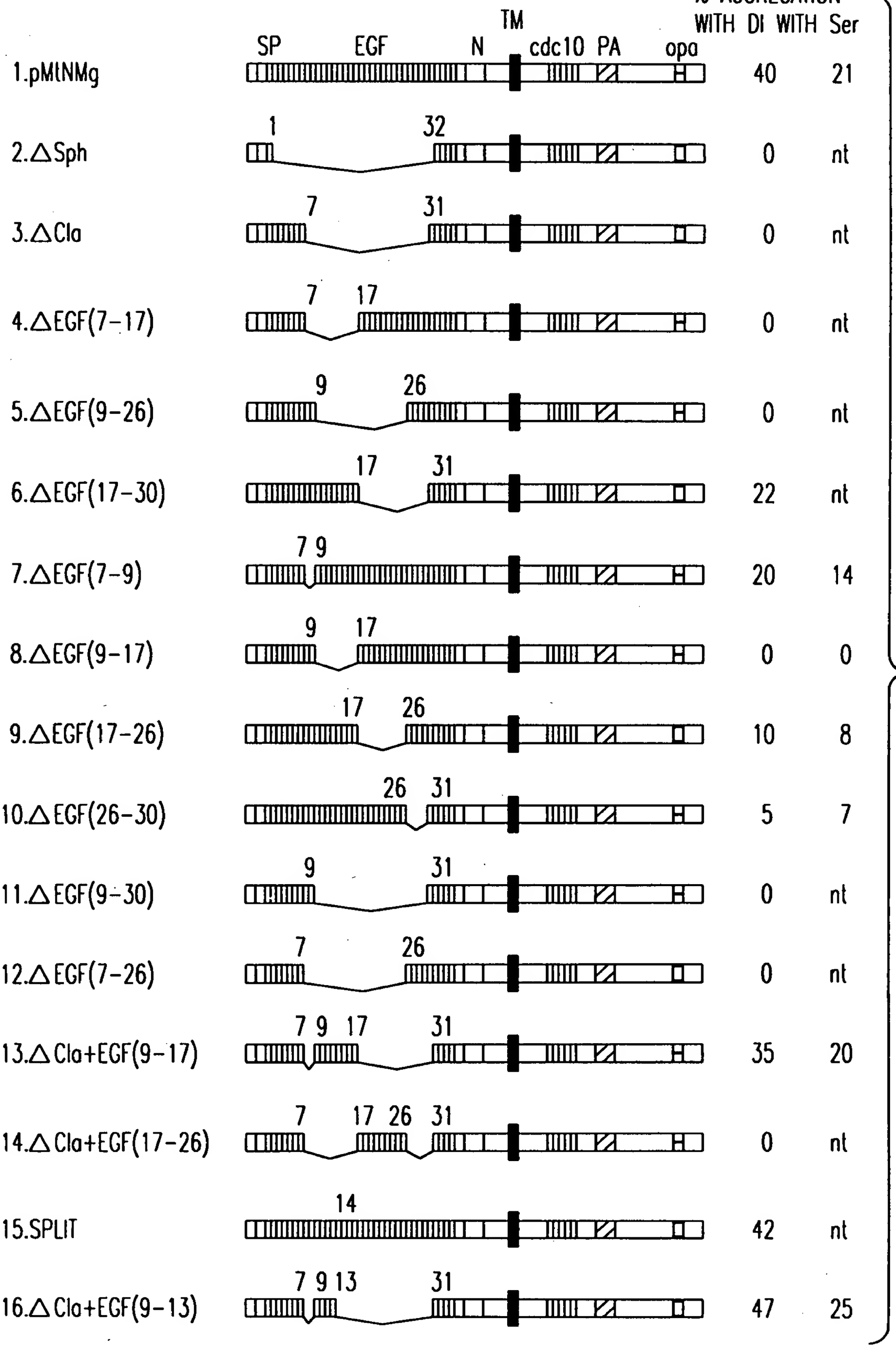


FIG.2A

17. △Cla+EGF(11-15)	7 11 15 31	0	0
18. △Cla+EGF(13-17)	7 13 17 31	0	nt
19. △Cla+EGF(10-13)	7 10 13 31	56	23
20. △Cla+EGF(11-13)	7 11 13 31	0	nt
21. △Cla+EGF(10-12)	7 10 12 31	0	nt
22. △Cla+EGF(10-11)	7 10 11 31	0	nt
23. △Cla+EGF(10-12)	7 10 12 31	45	nt
24. △Cla+EGF(11-12)	7 11 12 31	11	nt
25. △EGF	1	0	nt
26. △EGF+EGF(9-17)	1 9 17	24	nt
27. △EGF+EGF(9-13)	1 9 13	40	nt
28. △EGF+EGF(10-13)	1 10 13	45	23
29. △EGF+EGF(10-12)	1 10 12	48	nt
30. △ECN	1	0	nt
31. △ECN+EGF(10-13)	1 10 13	26	nt
32. △ECN+EGF(10-12)	1 10 12	47	22
33. △Cla+XEGF(10-13)	7 (10) (13) 31	42	20

FIG.2B

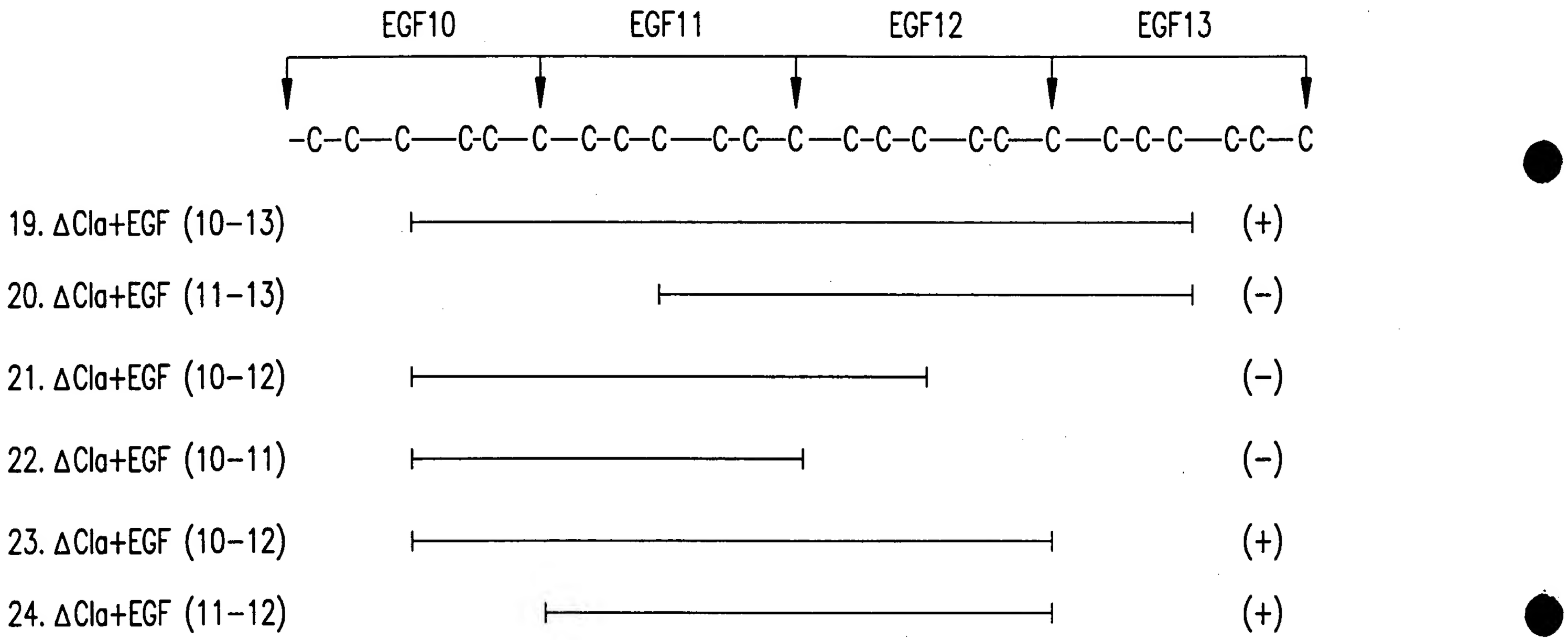


FIG.3

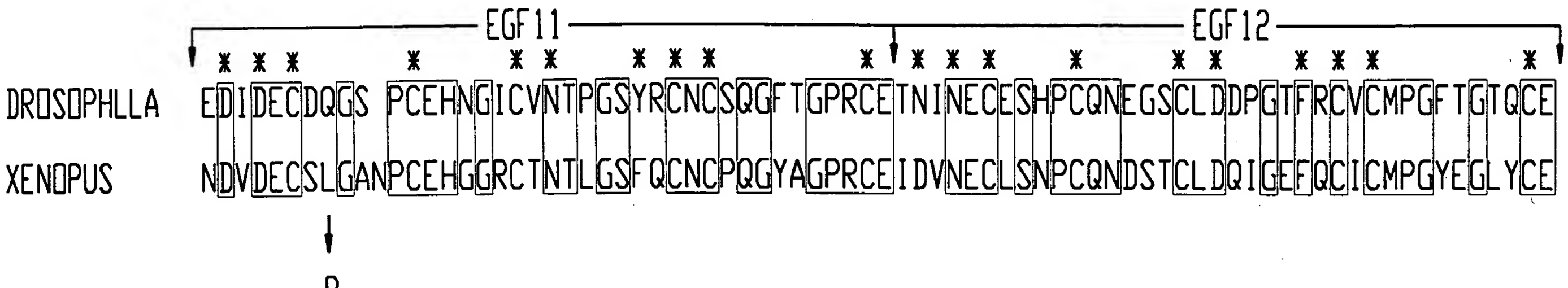


FIG.4

```
   1  CCGAGTCGAGCGCCGTGCTTCGAGCGGTGATGAGCCCCTTTTCTGTCAACGCTAAAGATC
 121  AAGCACATACTAAGGTCCATATAAATAATAAATAATAATTGTGTGTGATAACAACATTAT
 241  GGCCGTTATTCAGCTATCCAGAGCAAGTGTAGTGTGGCAAAATAGAAACAAACAAAGGCA
 361  CAATCCAGAGTGAATCCGAAACAAACTCCATCTAGATCGCCAACCAGCATCACGCTCGCA

 481  TCGTCGTTGGAGTCAACAATAGAATCAGCAGACAGCCTGGGAATGTCCAAGAAGACGGCG
      SerSerLeuGluSerThrIleGluSerAlaAspSerLeuGlyMetSerLysLysThrAla

 601  CGCGATTGTCGATCATTAAAGTCTGCCTGCAACTTAATTGCTTTAATTTTAATACTGTTA
      ArgAspCysArgSerLeuLysSerAlaCysAsnLeuIleAlaLeuIleLeuIleLeuLeu

 721  AACAGCCATCTACTCAACGGCTATTGCTGCGGCATGCCAGCGGAACTTAGGGCCACCAAG
      AsnSerHisLeuLeuAsnGlyTyrCysCysGlyMetProAlaGluLeuArgAlaThrLys

                                                          #2
 841  ACCGAGCAGGGTGCCAGCATATCCACGGGCTGTTCGTTTGGCAACGCCACCACCAAGATA
      ThrGluGlnGlyAlaSerIleSerThrGlyCysSerPheGlyAsnAlaThrThrLysIle

 961  ACGTTTCGTTGGACGAAGTCGTTTACGCTGATACTGCAGGCGTTGGATATGTACAACACA
      ThrPheArgTrpThrLysSerPheThrLeuIleLeuGlnAlaLeuAspMetTyrAsnThr
           #3
1081  TCGCCGGAGTGGAAGACGCTGGACCACATCGGGCGGAACGCGCGGATCACCTACCGTGTC
      SerProGluTrpLysThrLeuAspHisIleGlyArgAsnAlaArgIleThrTyrArgVal

1201  GACGATCAGTTCGGTCACTACGCCTGCGGCTCCGAGGGTCAGAAGCTCTGCCTGAATGGC
      AspAspGlnPheGlyHisTyrAlaCysGlySerGluGlyGlnLysLeuCysLeuAsnGly
```

FIG.5A

FIG.5B

```
TACAAAACATCAGCGCCTATCAAGTGGAAGTGTCAAGTGTGAACAAAACAAAAACGAGAG
CCAAACAAAACCAAACAAAACGAAGGCAAAGTGGAGAAAATGATACAGCATCCAGAGTAC
CCAAAATCTGCATACATGGGCTAATTAAGGCTGCCCAGCGAATTTACATTTGTGTGGTGC
AACGCCCCCAGAATGTACAAAATGTTTAGGAAACATTTTCGGCGAAAACCAGCTACGTCG
                        MetPheArgLysHisPheArgArgLysProAlaThrSer  13

ACAAAAAGGCAGCGTCCGAGGCATCGGGTACCCAAAATCGCGACCCTGCCATCGACGATC
ThrLysArgGlnArgProArgHisArgValProLysIleAlaThrLeuProSerThrIle  53

GTCCATAAGATATCCGCAGCTGGTAACTTCGAGCTGGAAATATTAGAAATCTCAAATACC
ValHisLysIleSerAlaAlaGlyAsnPheGluLeuGluIleLeuGluIleSerAsnThr  93
                                                    #1
ACGATAGGCTGCTCGCCATGCACGACGGCATTCCGGCTGTGCCTGAAGGAGTACCAGACC
ThrIleGlyCysSerProCysThrThrAlaPheArgLeuCysLeuLysGluTyrGlnThr  133

CTGGGTGGCTCCAGCTTTGTGCTCAGCGATCCGGGTGTGGGAGCCATTGTGCTGCCCTTT
LeuGlyGlySerSerPheValLeuSerAspProGlyValGlyAlaIleValLeuProPhe  173

TCCTATCCAGATGCGGAGAGGTTAATTGAGGAAACATCATACTCGGGCGTGATACTGCCG
SerTyrProAspAlaGluArgLeuIleGluGluThrSerTyrSerGlyValIleLeuPro  213
                                                        #4
CGGGTGCAATGCGCCGTTACCTACTACAACACGACCTGCACGACCTTCTGCCGTCCGCGG
ArgValGlnCysAlaValThrTyrTyrAsnThrThrCysThrThrPheCysArgProArg  253

TGGCAGGGCGTCAACTGCGAGGAGGCCATATGCAAGGCGGGCTGCGACCCCGTCCACGGC
TrpGlnGlyValAsnCysGluGluAlaIleCysLysAlaGlyCysAspProValHisGly  293
```

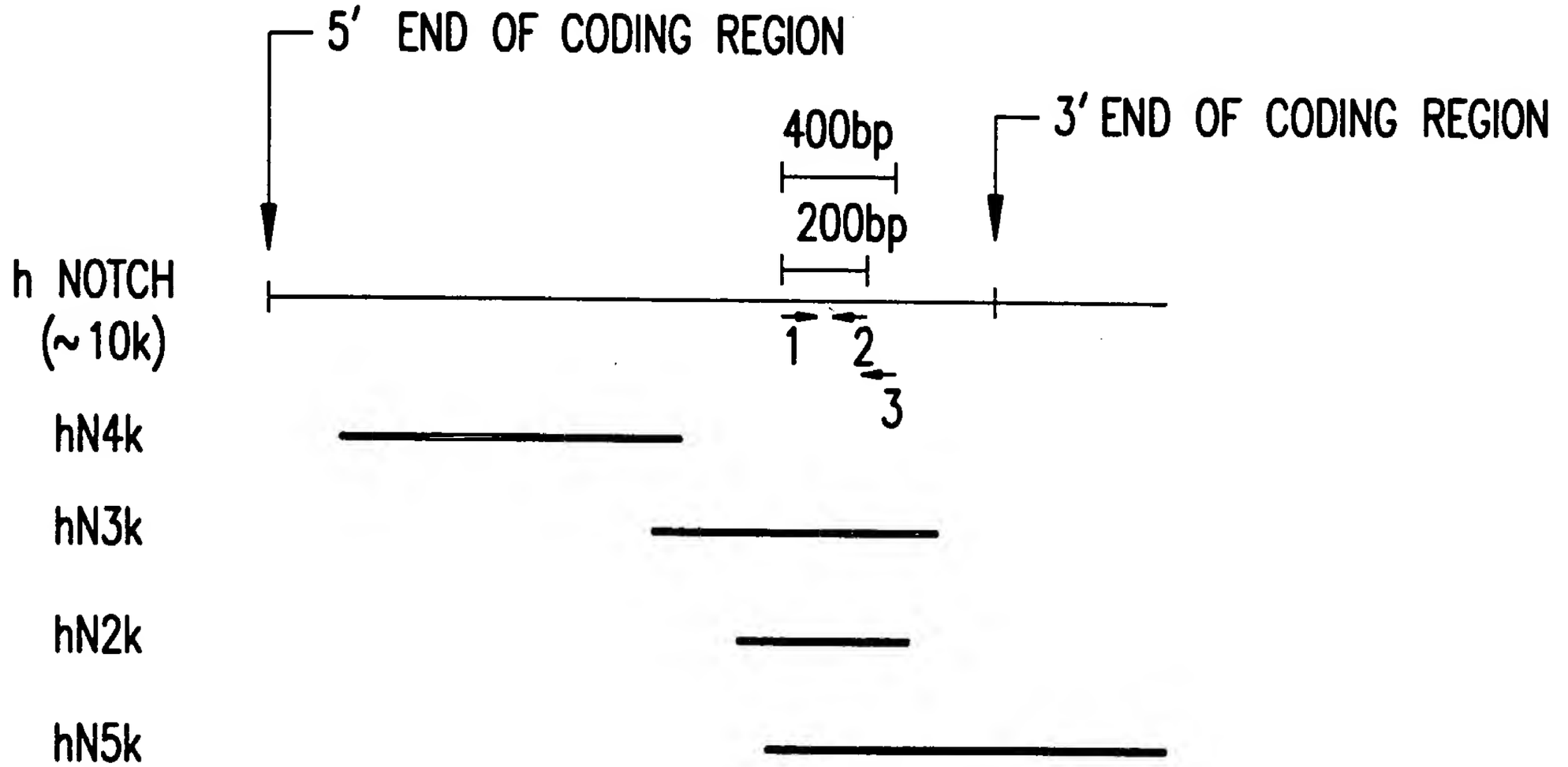


FIG.6

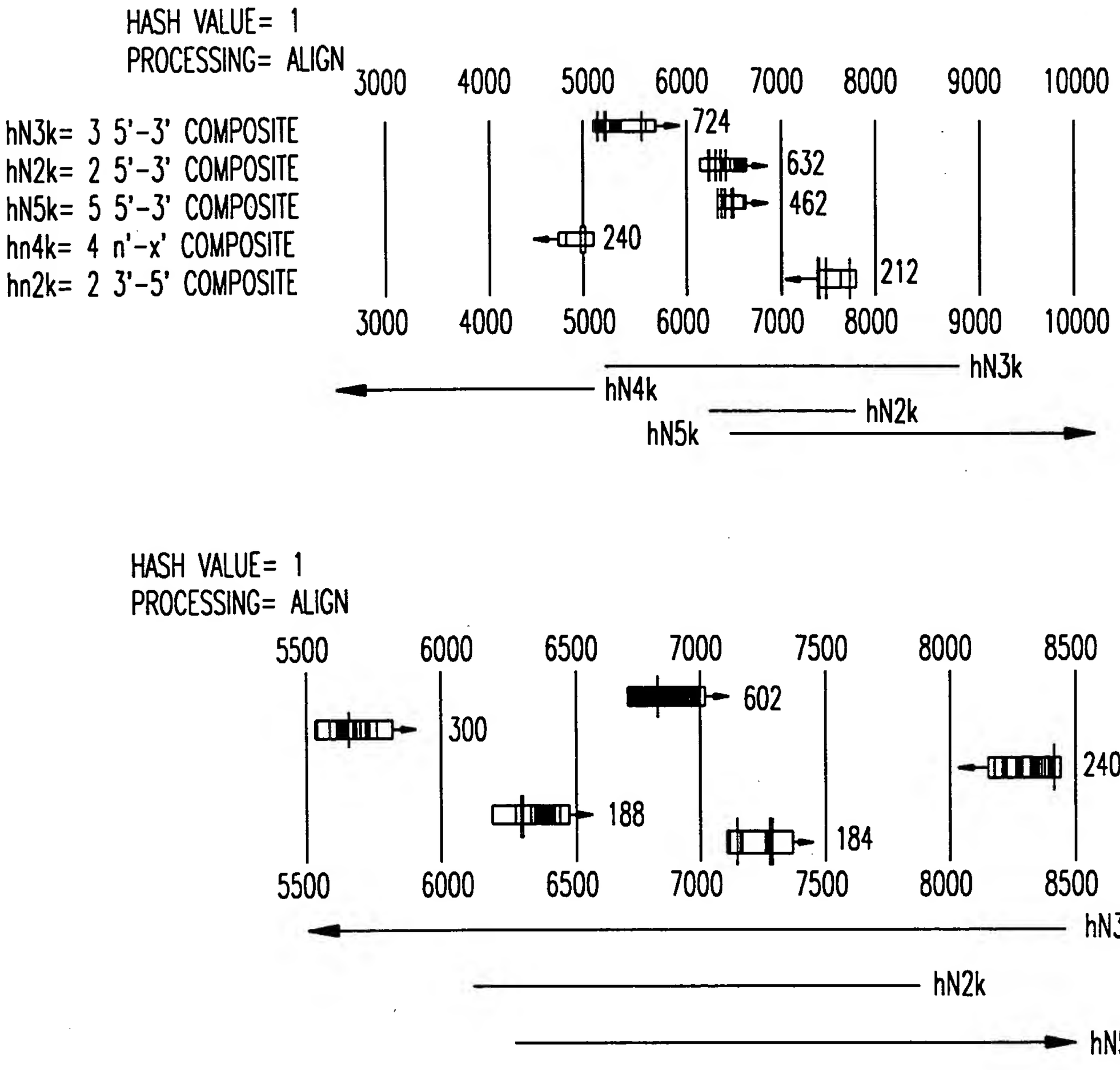


FIG.7

```
   1  GAATTCCGCT GGGAGAATGG TCTGAGCTAC CTGCCCGTCC TGCTGGGGCA TCAATGGCAA
  61  GTGGGGAAAG CCACACTGGG CAAACGGGCC AGGCCATTTC TGGAATGTGG TACATGGTGG
 121  GCAGGGGGCC CGCAACAGCT GGAGGGCAGG TGGACTGAGG CTGGGGATCC CCCGCTGGTT
 181  GGGCAATACT GCCTTTACCC ATGAGCTGGA AAGTCACAAT GGGGGGCAAG GGCTCCCGAG
 241  GGTGGTTATG TGCTTCCTTC AGGTGGC
```

FIG.8A

```
   1  GAATTCCTTC CATTATACGT GACTTTTCTG AAACTGTAGC CACCCTAGTG TCTCTAACTC
  61  CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GCTCCTTAAT
 121  GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC
 181  AACCCGGAAC TGAAGGCTGG CTCTCACCCT CTAGGCAGAG CAGGAATTCC GAGGTGGATG
 241  TGTTAGATGT GAATGTCCGT GGCCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCTCC
 301  GAGGAGGCAG CTCAGATTTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACA
 361  TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGAC CAGACAGACC GGACTGGTGA
 421  GATGGCCCTG CACCTTGCAG CCCGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA
 481  TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCCGC TGTCCACTCC ATGCTGCAGT
 541  GGCACGTGAT GCCAAGGTGT ATTCAGATCT GTTA
```

FIG.8B

```
   1  TCCAGATTCT GATTCGCAAC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA
  61  CACCCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT
 121  GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTCAC TGGGCAGCTG
 181  CTGTCAATAA TGTGGAGGCA ACTCTTTTGT TGTTGAAAAA TGGGGCCAAC CGAGACATGC
 241  AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCG GGAGGAGCTA TAAGC
```

FIG.8C

```
  1  GAATTCCATT CAGGAGGAAA GGGTGGGGAG AGAAGCAGGC ACCCACTTTC CCGTGGCTGG
 61  ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CGGAGTGCCA
121  TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA
181  GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG
241  CAGAGCTG
```

FIG.9A

```
  1  CTAAAGGGAA CAAAAGCNGG AGCTCCACCG CGGGCGGCNC NGCTCTAGAA CTAGTGGANN
 61  NCCCGGGCTG CAGGAATTCC GGCGGACTGG GCTCGGGCTC AGAGCGGCGC TGTGGAAGAG
121  ATTCTAGACC GGGAGAACAA GCGAATGGCT GACAGCTGGC CTCCAAAGTC ACCAGGCTCA
181  AATCGCTCGC CCTGGACATC GAGGGATGCA GAGGATCAGA ACCGGTACCT GGATGGCATG
241  ACTCGGATTT ACAAGCATGA CCAGCCTGCT TACAGGGAGC GTGANNTTTT CACATGCAGT
301  CGACAGACAC GAGCTCTATG CAT
```

FIG.9B

```
          10          20          30          40
     *    *    *    *    *    *    *    *    *
TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC
 C   Q   E   D   A   G   N   K   V   C   S   L   Q   C   N   N>

50          60          70          80          90
 *    *    *    *    *    *    *    *    *    *    *
CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC
 H   A   C   G   W   D   G   G   D   C   S   L   N   F   N   D>

  100         110         120         130         140
     *    *    *    *    *    *    *    *    *    *
CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT
 P   W   K   N   C   T   Q   S   L   Q   C   W   K   Y   F   S>

    150         160         170         180         190
*    *    *    *    *    *    *    *    *    *    *
GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC
 D   G   H   C   D   S   Q   C   N   S   A   G   C   L   F   D>
```

FIG. 10A

```
      200         210         220         230         240
       *   *   *   *   *   *   *   *   *   *   *   *
GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC
 G   F   D   C   Q   R   A   E   G   Q   C   N   P   L   Y   D> -

          250         260         270         280
       *   *   *   *   *   *   *   *   *   *   *
CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC
 Q   Y   C   K   D   H   F   S   D   G   H   C   D   Q   G   C>

290         300         310         320         330
 *   *   *   *   *   *   *   *   *   *   *   *
AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA
 N   S   A   E   C   E   W   D   G   L   D   C   A   E   H   V>

  340         350         360         370         380
    *   *   *   *   *   *   *   *   *   *   *
CCC GAG AGG CTG GCG GCC GGC ACG CTG GTG GTG GTG GTG CTG ATG CCG
 P   E   R   L   A   A   G   T   L   V   V   V   V   L   M   P>
```

FIG.10B

```
     390          400          410          420          430
*    *    *    *    *    *    *    *    *    *    *    *
CCG GAG CAG CTG CGC AAC AGC TCC TTC CAC TTC CTG CGG GAG CTC AGC
 P   E   Q   L   R   N   S   S   F   H   F   L   R   E   L   S>

        440          450          460          470          480
  *    *    *    *    *    *    *    *    *    *    *    *    *
CGC GTG CTG CAC ACC AAC GTG GTC TTC AAG CGT GAC GCA CAC GGC CAG
 R   V   L   H   T   N   V   V   F   K   R   D   A   H   G   Q>

             490          500          510          520
     *    *    *    *    *    *    *    *    *    *    *
CAG ATG ATC TTC CCC TAC TAC GGC CGC GAG GAG GAG CTG CGC AAG CAC
 Q   M   I   F   P   Y   Y   G   R   E   E   E   L   R   K   H>

530          540          550          560          570
  *    *    *    *    *    *    *    *    *    *    *    *
CCC ATC AAG CGT GCC GCC GAG GGC TGG GCC GCA CCT GAC GCC CTG CTG
 P   I   K   R   A   A   E   G   W   A   A   P   D   A   L   L>
```

FIG. 10C

```
  580          590          600          610          620
    *    *       *    *       *    *       *    *       *
GGC CAG GTG AAG GCC TCG CTG CTC CCT GGT GGC AGC GAG GGT GGG CGG
 G   Q   V   K   A   S   L   L   P   G   G   S   E   G   G   R>

    630          640          650          660          670
*    *       *    *       *    *       *    *       *    *
CGG CGG AGG GAG CTG GAC CCC ATG GAC GTC CGC GGC TCC ATC GTC TAC
 R   R   R   E   L   D   P   M   D   V   R   G   S   I   V   Y>

      680          690          700          710          720
  *    *       *    *       *    *       *    *       *    *
CTG GAG ATT GAC AAC CGG CAG TGT GTG CAG GCC TCC TCG CAG TGC TTC
 L   E   I   D   N   R   Q   C   V   Q   A   S   S   Q   C   F>

        730          740          750          760
    *    *       *    *       *    *       *    *
CAG AGT GCC ACC GAC GTG GCC GCA TTC CTG GGA GCG CTC GCC TCG CTG
 Q   S   A   T   D   V   A   A   F   L   G   A   L   A   S   L>
```

FIG. 10D

```
770               780               790               800               810
  *       *       *       *       *       *       *       *       *       *
 GGC AGC CTC AAC ATC CCC TAC AAG ATC GAG GCC GTG CAG AGT GAG ACC
  G   S   L   N   I   P   Y   K   I   E   A   V   Q   S   E   T>-

   820               830               840               850               860
     *       *       *       *       *       *       *       *       *
 GTG GAG CCG CCC CCG CCG GCG CAG CTG CAC TTC ATG TAC GTG GCG GCG
  V   E   P   P   P   P   A   Q   L   H   F   M   Y   V   A   A>

     870               880               890               900               910
*       *       *       *       *       *       *       *       *       *
GCC GCC TTT GTG CTT CTG TTC TTC GTG GGC TGC GGG GTG CTG CTG TCC
 A   A   F   V   L   L   F   F   V   G   C   G   V   L   L   S>

         920               930               940               950               960
   *       *       *       *       *       *       *       *       *       *
CGC AAG CGC CGG CGG CAG CAT GGC CAG CTC TGG TTC CCT GAG GGC TTC
 R   K   R   R   R   Q   H   G   Q   L   W   F   P   E   G   F>
```

FIG.10E

```
          970         980         990        1000
      *     *     *     *     *     *     *     *     *
AAA GTG TCT GAG GCC AGC AAG AAG AAG CGG CGG GAG CCC CTC GGC GAG
 K   V   S   E   A   S   K   K   K   R   R   E   P   L   G   E>

1010        1020        1030        1040        1050
   *     *     *     *     *     *     *     *     *     *
GAC TCC GTG GGC CTC AAG CCC CTG AAG AAC GCT TCA GAC GGT GCC CTC
 D   S   V   G   L   K   P   L   K   N   A   S   D   G   A   L>

 1060        1070        1080        1090        1100
    *     *     *     *     *     *     *     *     *
ATG GAC GAC AAC CAG AAT GAG TGG GGG GAC GAG GAC CTG GAG ACC AAG
 M   D   D   N   Q   N   E   W   G   D   E   D   L   E   T   K>

   1110        1120        1130        1140        1150
*     *     *     *     *     *     *     *     *     *
AAG TTC CGG TTC GAG GAG CCC GTG GTT CTG CCT GAC CTG GAC GAC CAG
 K   F   R   F   E   E   P   V   V   L   P   D   L   D   D   Q>
```

FIG.10F

```
      1160          1170          1180          1190          1200
       *     *       *     *       *     *       *     *       *     *

ACA GAC CAC CGG CAG TGG ACT CAG CAG CAC CTG GAT GCC GCT GAC CTG
 T   D   H   R   Q   W   T   Q   Q   H   L   D   A   A   D   L>

          1210          1220          1230          1240
       *     *       *     *       *     *       *     *       *

CGC ATG TCT GCC ATG GCC CCC ACA CCG CCC CAG GGT GAG GTT GAC GCC
 R   M   S   A   M   A   P   T   P   P   Q   G   E   V   D   A>

1250          1260          1270          1280          1290
 *     *       *     *       *     *       *     *       *     *

GAC TGC ATG GAC GTC AAT GTC CGC GGG CCT GAT GGC TTC ACC CCG CTC
 D   C   M   D   V   N   V   R   G   P   D   G   F   T   P   L>

1300          1310          1320          1330          1340
    *     *       *     *       *     *       *     *       *

ATG ATC GCC TCC TGC AGC GGG GGC GGC CTG GAG ACG GGC AAC AGC GAG
 M   I   A   S   C   S   G   G   G   L   E   T   G   N   S   E>
```

FIG. 10G

```
   1350          1360          1370          1380          1390
*     *       *     *     *     *     *     *     *     *
GAA GAG GAG GAC GCG CCG GCC GTC ATC TCC GAC TTC ATC TAC CAG GGC
 E   E   E   D   A   P   A   V   I   S   D   F   I   Y   Q   G>

      1400          1410          1420          1430          1440
  *     *       *     *     *     *     *     *     *     *     *
GCC AGC CTG CAC AAC CAG ACA GAC CGC ACG GGC GAG ACC GCC TTG CAC
 A   S   L   H   N   Q   T   D   R   T   G   E   T   A   L   H>

          1450          1460          1470          1480
      *     *       *     *     *     *     *     *     *     *
  CTG GCC GCC CGC TAC TCA CGC TCT GAT GCC GCC AAG CGC CTG CTG GAG
   L   A   A   R   Y   S   R   S   D   A   A   K   R   L   L   E>

1490          1500          1510          1520          1530
   *     *       *     *     *     *     *     *     *     *
  GCC AGC GCA GAT GCC AAC ATC CAG GAC AAC ATG GGC CGC ACC CCG CTG
   A   S   A   D   A   N   I   Q   D   N   M   G   R   T   P   L>
```

FIG. 10H

```
 1540          1550          1560          1570          1580
    *     *       *     *       *     *       *     *       *
CAT GCG GCT GTG TCT GCC GAC GCA CAA GGT GTC TTC CAG ATC CTG ATC
 H   A   A   V   S   A   D   A   Q   G   V   F   Q   I   L   I>

   1590          1600          1610          1620          1630
*     *       *     *       *     *       *     *       *     *
CGG AAC CGA GCC ACA GAC CTG GAT GCC CGC ATG CAT GAT GGC ACG ACG
 R   N   R   A   T   D   L   D   A   R   M   H   D   G   T   T>

      1640          1650          1660          1670          1680
  *     *       *     *       *     *       *     *       *     *
CCA CTG ATC CTG GCT GCC CGC CTG GCC GTG GAG GGC ATG CTG GAG GAC
 P   L   I   L   A   A   R   L   A   V   E   G   M   L   E   D>

          1690          1700          1710          1720
     *     *       *     *       *     *       *     *
CTC ATC AAC TCA CAC GCC GAC GTC AAC GCC GTA GAT GAC CTG GGC AAG
 L   I   N   S   H   A   D   V   N   A   V   D   D   L   G   K>

1730          1740          1750          1760          1770
   *     *       *     *       *     *       *     *       *
TCC GCC CTG CAC TGG GCC GCC GCC GTG AAC AAT GTG GAT GCC GCA GTT
 S   A   L   H   W   A   A   A   V   N   N   V   D   A   A   V>
```

FIG. 10I

```
 1780          1790          1800          1810          1820
    *     *       *     *       *     *       *     *       *
GTG CTC CTG AAG AAC GGG GCT AAC AAA GAT ATG CAG AAC AAC AGG GAG
 V   L   L   K   N   G   A   N   K   D   M   Q   N   N   R   E>

   1830          1840          1850          1860          1870
*     *       *     *       *     *       *     *       *     *
GAG ACA CCC CTG TTT CTG GCC GCC CGG GAG GGC AGC TAC GAG ACC GCC
 E   T   P   L   F   L   A   A   R   E   G   S   Y   E   T   A>

     1880          1890          1900          1910          1920
  *     *       *     *       *     *       *     *       *     *
AAG GTG CTG CTG GAC CAC TTT GCC AAC CGG GAC ATC ACG GAT CAT ATG
 K   V   L   L   D   H   F   A   N   R   D   I   T   D   H   M>

         1930          1940          1950          1960
     *     *       *     *       *     *       *     *
GAC CGC CTG CCG CGC GAC ATC GCA CAG GAG CGC ATG CAT CAC GAC ATC
 D   R   L   P   R   D   I   A   Q   E   R   M   H   H   D   I>
```

FIG. 10J

```
1970          1980          1990          2000          2010
   *     *     *     *     *     *     *     *     *     *
GTG AGG CTG CTG GAC GAG TAC AAC CTG GTG CGC AGC CCG CAG CTG CAC
 V   R   L   L   D   E   Y   N   L   V   R   S   P   Q   L   H>

2020          2030          2040          2050          2060
   *     *     *     *     *     *     *     *     *
GGA GCC CCG CTG GGG GGC ACG CCC ACC CTG TCG CCC CCG CTC TGC TCG
 G   A   P   L   G   G   T   P   T   L   S   P   P   L   C   S>

2070          2080          2090          2100          2110
*     *     *     *     *     *     *     *     *     *
CCC AAC GGC TAC CTG GGC AGC CTC AAG CCC GGC GTG CAG GGC AAG AAG
 P   N   G   Y   L   G   S   L   K   P   G   V   Q   G   K   K>

2120          2130          2140          2150          2160
  *     *     *     *     *     *     *     *     *     *
GTC CGC AAG CCC AGC AGC AAA GGC CTG GCC TGT GGA AGC AAG GAG GCC
 V   R   K   P   S   S   K   G   L   A   C   G   S   K   E   A>
```

FIG. 10K

```
          2170          2180          2190          2200
      *     *     *     *     *     *     *     *     *
AAG GAC CTC AAG GCA CGG AGG AAG AAG TCC CAG GAT GGC AAG GGC TGC
 K   D   L   K   A   R   R   K   K   S   Q   D   G   K   G   C>

2210          2220          2230          2240          2250
  *     *     *     *     *     *     *     *     *     *
CTG CTG GAC AGC TCC GGC ATG CTC TCG CCC GTG GAC TCC CTG GAG TCA
 L   L   D   S   S   G   M   L   S   P   V   D   S   L   E   S>

  2260          2270          2280          2290          2300
    *     *     *     *     *     *     *     *     *     *
CCC CAT GGC TAC CTG TCA GAC GTG GCC TCG CCG CCA CTG CTG CCC TCC
 P   H   G   Y   L   S   D   V   A   S   P   P   L   L   P   S>

   2310          2320          2330          2340          2350
*     *     *     *     *     *     *     *     *     *     *
CCG TTC CAG CAG TCT CCG TCC GTG CCC CTC AAC CAC CTG CCT GGG ATG
 P   F   Q   Q   S   P   S   V   P   L   N   H   L   P   G   M>
```

FIG.10L

```
      2360          2370          2380          2390          2400
       *     *       *     *       *     *       *     *       *
CCC GAC ACC CAC CTG GGC ATC GGG CAC CTG AAC GTG GCG GCC AAG CCC
 P   D   T   H   L   G   I   G   H   L   N   V   A   A   K   P>

            2410          2420          2430          2440
         *     *       *     *       *     *       *     *
GAG ATG GCG GCG CTG GGT GGG GGC GGC CGG CTG GCC TTT GAG ACT GGC
 E   M   A   A   L   G   G   G   G   R   L   A   F   E   T   G>

2450          2460          2470          2480          2490
   *     *       *     *       *     *       *     *       *
CCA CCT CGT CTC TCC CAC CTG CCT GTG GCC TCT GGC ACC AGC ACC GTC
 P   P   R   L   S   H   L   P   V   A   S   G   T   S   T   V>

 2500          2510          2520          2530          2540
    *     *       *     *       *     *       *     *       *
CTG GGC TCC AGC AGC GGA GGG GCC CTG AAT TTC ACT GTG GGC GGG TCC
 L   G   S   S   S   G   G   A   L   N   F   T   V   G   G   S>
```

FIG.10M

```
   2550          2560          2570          2580          2590
*     *       *     *     *     *     *     *     *     *     *
ACC AGT TTG AAT GGT CAA TGC GAG TGG CTG TCC CGG CTG CAG AGC GGC
 T   S   L   N   G   Q   C   E   W   L   S   R   L   Q   S   G>

      2600          2610          2620          2630          2640
  *     *       *     *     *     *     *     *     *     *     *
ATG GTG CCG AAC CAA TAC AAC CCT CTG CGG GGG AGT GTG GCA CCA GGC
 M   V   P   N   Q   Y   N   P   L   R   G   S   V   A   P   G>

          2650          2660          2670          2680
      *     *       *     *     *     *     *     *     *     *
  CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG
   P   L   S   T   Q   A   P   S   L   Q   H   G   M   V   G   P>

2690          2700          2710          2720          2730
   *     *       *     *     *     *     *     *     *     *
  CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC
   L   H   S   S   L   A   A   S   A   L   S   Q   M   M   S   Y>
```

FIG. 10N

```
 2740          2750          2760          2770          2780
    *     *       *     *       *     *       *     *       *
CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CCT CAC CTG GTG CAG
 Q   G   L   P   S   T   R   L   A   T   Q   P   H   L   V   Q>

   2790          2800          2810          2820          2830
*     *       *     *       *     *       *     *       *     *
ACC CAG CAG GTG CAG CCA CAA AAC TTA CAG ATG CAG CAG CAG AAC CTG
 T   Q   Q   V   Q   P   Q   N   L   Q   M   Q   Q   Q   N   L>

      2840          2850          2860          2870          2880
  *     *       *     *       *     *       *     *       *     *
CAG CCA GCA AAC ATC CAG CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA
 Q   P   A   N   I   Q   Q   Q   Q   S   L   Q   P   P   P   P>

          2890          2900          2910          2920
      *     *       *     *       *     *       *     *       *
CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG
 P   P   Q   P   H   L   G   V   S   S   A   A   S   G   H   L>

2930          2940          2950          2960          2970
   *     *       *     *       *     *       *     *       *     *
GGC CGG AGC TTC CTG AGT GGA GAG CCG AGC CAG GCA GAC GTG CAG CCA

 G   R   S   F   L   S   G   E   P   S   Q   A   D   V   Q   P>
```

FIG. 10 O

```
 2980          2990          3000          3010          3020
    *     *       *     *       *     *       *     *       *
CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC
 L   G   P   S   S   L   A   V   H   T   I   L   P   Q   E   S>

   3030          3040          3050          3060          3070
*     *       *     *       *     *       *     *       *     *
CCC GCC CTG CCC ACG TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC
 P   A   L   P   T   S   L   P   S   S   L   V   P   P   V   T>

      3080          3090          3100          3110          3120
   *     *       *     *       *     *       *     *       *     *
GCA GCC CAG TTC CTG ACG CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT
 A   A   Q   F   L   T   P   P   S   Q   H   S   Y   S   S   P>
```

FIG. 10P

```
          3130          3140          3150          3160
        *     *     *     *     *     *     *     *     *
GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG
 V   D   N   T   P   S   H   Q   L   Q   V   P   V   P   V   M>

3170          3180          3190          3200          3210
  *     *     *     *     *     *     *     *     *     *
GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA TCA ATT TTG ATC
 V   M   I   R   S   S   D   P   S   K   G   S   S   I   L   I>

3220          3230
    *     *     *
GAA GCT CCC GAC TCA TGG
 E   A   P   D   S   W>
```

FIG. 10Q

```
G GAG GTG GAT GTG TTA GAT GTG AAT GTC CGT GGC CCA GAT GGC TGC      46
  Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys
    1               5                  10                  15

ACC CCA TTG ATG TTG GCT TCT CTC CGA GGA GGC AGC TCA GAT TTG AGT    94
Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser
                  20                  25                  50

GAT GAA GAT GAA GAT GCA GAG GAC TCT TCT GCT AAC ATC ATC ACA GAC    142
Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp
            35                  40                  45

TTG GTC TAC CAG GGT GCC AGC CTC CAG GCC CAG ACA GAC CGG ACT GGT    190
Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly
      50                  55                  60

GAG ATG GCC CTG CAC CTT GCA GCC CGC TAC TCA CGG GCT GAT GCT GCC    238
Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala
  65                  70                  75

AAG CGT CTC CTG GAT GCA GGT GCA GAT GCC AAT GCC CAG GAC AAC ATG    286
Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met
80                  85                  90                  95

GGC CGC TGT CCA CTC CAT GCT GCA GTG GCA GCT GAT GCC CAA GGT GTC    334
Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val
              100                 105                 110

TTC CAG ATT CTG ATT CGC AAC CGA GTA ACT GAT CTA GAT GCC AGG ATG    382
Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met
            115                 120                 125

AAT GAT GGT ACT ACA CCC CTG ATC CTG GCT GCC CGC CTG GCT GTG GAG    430
Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu
      130                 135                 140
```

FIG.11A

```
GGA ATG GTG GCA GAA CTG ATC AAC TGC CAA GCG GAT GTG AAT GCA GTG     478
Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val
    145                 150                 155

GAT GAC CAT GGA AAA TCT GCT CTT CAC TGG GCA GCT GCT GTC AAT AAT     526
Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn
160                 165                 170                 175

GTG GAG GCA ACT CTT TTG TTG TTG AAA AAT GGG GCC AAC CGA GAC ATG     574
Val Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met
                180                 185                 190

CAG GAC AAC AAG GAA GAG ACA CCT CTG TTT CTT GCT GCC CGG GAG GGG     622
Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly
            195                 200                 205

AGC TAT GAA GCA GCC AAG ATC CTG TTA GAC CAT TTT GCC AAT CGA GAC     670
Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp
        210                 215                 220

ATC ACA GAC CAT ATG GAT CGT CTT CCC CGG GAT GTG GCT CGG GAT CGC     718
Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg
    225                 230                 235

ATG CAC CAT GAC ATT GTG CGC CTT CTG GAT GAA TAC AAT GTG ACC CCA     766
Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro
240                 245                 250                 255

AGC CCT CCA GGC ACC GTG TTG ACT TCT GCT CTC TCA CCT GTC ATC TGT     814
Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys
                260                 265                 270

GGG CCC AAC AGA TCT TTC CTC AGC CTG AAG CAC ACC CCA ATG GGC AAG     862
Gly Pro Asn Arg Ser Phe Leu Ser Leu Lyn His Thr Pro Met Gly Lys
            275                 280                 285
```

FIG.11B

```
AAG TCT AGA CGG CCC AGT GCC AAG AGT ACC ATG CCT ACT AGC CTC CCT   910
Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser Leu Pro
        290                 295                 300

AAC CTT GCC AAG GAG GCA AAG GAT GCC AAG GGT AGT AGG AGG AAG AAG   958
Asn Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys
    305                 310                 315

TCT CTG AGT GAG AAG GTC CAA CTG TCT GAG AGT TCA GTA ACT TTA TCC  1006
Ser Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Ser Val Thr Leu Ser
320                 325                 330                 335

CCT GTT GAT TCC CTA GAA TCT CCT CAC ACG TAT GTT TCC GAC ACC ACA  1054
Pro Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr
                340                 345                 350

TCC TCT CCA ATG ATT ACA TCC CCT GGG ATC TTA CAG GCC TCA CCC AAC  1102
Ser Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn
            355                 360                 365

CCT ATG TTG GCC ACT GCC GCC CCT CCT GCC CCA GTC CAT GCC CAG CAT  1150
Pro Met Leu Ala Thr Ala Ala Pro Pro Ala Pro Val His Ala Gln His
        370                 375                 380

GCA CTA TCT TTT TCT AAC CTT CAT GAA ATG CAG CCT TTG GCA CAT GGG  1198
Ala Leu Ser Phe Ser Asn Leu His Glu Met Gln Pro Leu Ala His Gly
    385                 390                 395

GCC AGC ACT GTG CTT CCC TCA GTG AGC CAG TTG CTA TCC CAC CAC CAC  1246
Ala Ser Thr Val Leu Pro Ser Val Ser Gln Leu Leu Ser His His His
400                 405                 410                 415

ATT GTG TCT CCA GGC AGT GGC AGT GCT GGA AGC TTG AGT AGG CTC CAT  1294
Ile Val Ser Pro Gly Ser Gly Ser Ala Gly Ser Leu Ser Arg Leu His
                420                 425                 430

CCA GTC CCA GTC CCA GCA GAT TGG ATG AAC CGC ATG GAG GTG AAT GAG  1342
Pro Val Pro Val Pro Ala Asp Trp Met Asn Arg Met Glu Val Asn Glu
            435                 440                 445
```

FIG.11C

```
ACC CAG TAC AAT GAG ATG TTT GGT ATG GTC CTG GCT CCA GCT GAG GGC  1390
Thr Gln Tyr Asn Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu Gly
        450                 455                 460

ACC CAT CCT GGC ATA GCT CCC CAG AGC AGG CCA CCT GAA GGG AAG CAC  1438
Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly Lys His
    465                 470                 475

ATA ACC ACC CCT CGG GAG CCC TTG CCC CCC ATT GTG ACT TTC CAG CTC  1486
Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu
480                 485                 490                 495

ATC CCT AAA GGC AGT ATT GCC CAA CCA GCG GGG GCT CCC CAG CCT CAG  1534
Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln
                500                 505                 510

TCC ACC TGC CCT CCA GCT GTT GCG GGC CCC CTG CCC ACC ATG TAC CAG  1582
Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu Pro Thr Met Tyr Gln
            515                 520                 525

ATT CCA GAA ATG GCC CGT TTG CCC AGT GTG GCT TTC CCC ACT GCC ATG  1630
Ile Pro Glu Met Ala Arg Leu Pro Ser Val Ala Phe Pro Thr Ala Met
        530                 535                 540

ATG CCC CAG CAG GAC GGG CAG GTA GCT CAG ACC ATT CTC CCA GCC TAT  1678
Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr
    545                 550                 555

CAT CCT TTC CCA GCC TCT GTG GGC AAG TAC CCC ACA CCC CCT TCA CAG  1726
His Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Gln
560                 565                 570                 575

CAC AGT TAT GCT TCC TCA AAT GCT GCT GAG CGA ACA CCC AGT CAC AGT  1774
His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser
                580                 585                 590

GGT CAC CTC CAG GGT GAG CAT CCC TAC CTG ACA CCA TCC CCA GAG TCT  1822
Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser
            595                 600                 605
```

FIG.11D

CCT GAC CAG TGG TCA AGT TCA TCA CCC CAC TCT GCT TCT GAC TGG TCA 1870
Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser
610 615 620

GAT GTG ACC ACC AGC CCT ACC CCT GGG GGT GCT GGA GGA GGT CAG CGG 1918
Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg
625 630 635

GGA CCT GGG ACA CAC ATG TCT GAG CCA CCA CAC AAC AAC ATG CAG GTT 1966
Gly Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val
640 645 650 655

TAT GCG TGAGAGAGTC CACCTCCAGT GTAGAGACAT AACTGACTTT TGTAAATGCT 2022
Tyr Ala

GCTGAGGAAC AAATGAAGGT CATCCGGGAG AGAAATGAAG AAATCTCTGG AGCCAGCTTC 2082

TAGAGGTAGG AAAGAGAAGA TGTTCTTATT CAGATAATGC AAGAGAAGCA ATTCGTCAGT 2142

TTCACTGGGT ATCTGCAAGG CTTATTGATT ATTCTAATCT AATAAGACAA GTTTGTGGAA 2202

ATGCAAGATG AATACAAGCC TTGGGTCCAT GTTTACTCTC TTCTATTTGG AGAATAAGAT 2262

GGATGCTTAT TGAAGCCCAG ACATTCTTGC AGCTTGGACT GCATTTTAAG CCCTGCAGGC 2322

TTCTGCCATA TCCATGAGAA GATTCTACAC TAGCGTCCTG TTGGGAATTA TGCCCTGGAA 2382

TTCTGCCTGA ATTGACCTAC GCATCTCCTC CTCCTTGGAC ATTCTTTTGT CTTCATTTGG 2442

TGCTTTTGGT TTTGCACCTC TCCGTGATTG TAGCCCTACC AGCATGTTAT AGGGCAAGAC 2502

CTTTGTGCTT TTGATCATTC TGGCCCATGA AAGCAACTTT GGTCTCCTTT CCCCTCCTGT 2562

CTTCCCGGTA TCCCTTGGAG TCTCACAAGG TTTACTTTGG TATGGTTCTC AGCACAAACC 2622

TTTCAAGTAT GTTGTTTCTT TGGAAAATGG ACATACTGTA TTGTGTTCTC CTGCATATAT 2682

CATTCCTGGA GAGAGAAGGG GAGAAGAATA CTTTTCTTCA ACAAATTTTG GGGGCAGGAG 2742

ATCCCTTCAA GAGGCTGCAC CTTAATTTTT CTTGTCTGTG TGCAGGTCTT CATATAAACT 2802

FIG.11E

TTACCAGGAA GAAGGGTGTG AGTTTGTTGT TTTTCTGTGT ATGGGCCTGG TCAGTGTAAA 2862

GTTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTTTAAAA CCAGAAAAAG 2922

GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC 2982

CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT 3042

CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT 3102

AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG 3162

CCATTTAGGA CTGAACTTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT 3222

CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282

TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342

TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402

CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462

TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522

FIG.11F

AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582

TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642

TCTTTGACTT TCTTTTAAGG GCAGAAGCAT TTTAGTTAAT TGTAGATAAA GAATAGTTTT 3702

CTTCCTCTTC TCCTTGGGCC AGTTAATAAT TGGTCCATGG CTACACTGCA ACTTCCGTCC 3762

AGTGCTGTGA TGCCCATGAC ACCTGCAAAA TAAGTTCTGC CTGGGCATTT TGTAGATATT 3822

AACAGGTGAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCCTT CTATGGCTGC 3882

AAGTATGCAT CAGTGCTTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAAC 3942

CCTGCGTGTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCCTAT CCAAATTTAT 4002

TGAACCAACA AAAATAATTA CTTCTGCCCT GAGATAAGCA GATTAAGTTT GTTCATTCTC 4062

TGCTTTATTC TCTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATTT 4122

TATCATTCTA AATGGTGACT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA 4182

ACCTATCTGC ATGGACCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG 4242

GCGATGGCGA TGACTTTCTT CCCCTG 4268

FIG. 11G

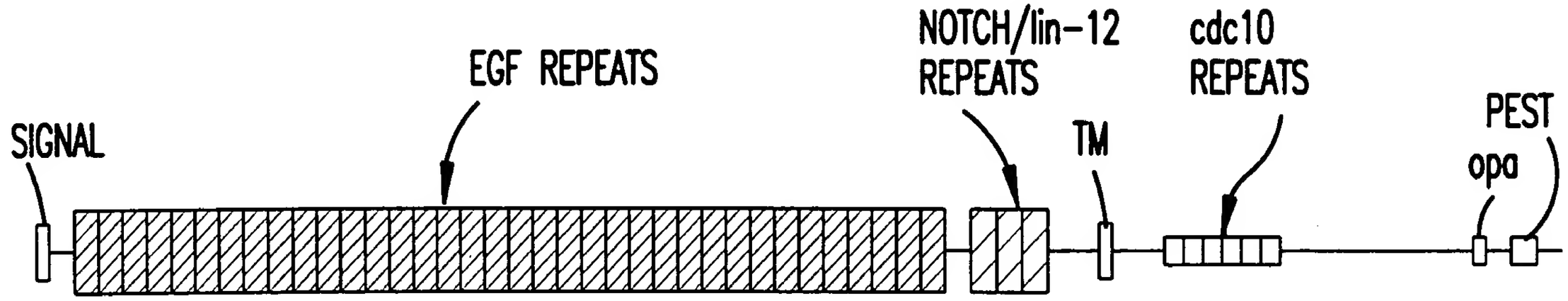


FIG.12A

CDC10-1 CDC10 REGION CDC10-2

hN5k		TPPQAEQEVDVL--DVNVRGPDGCTPLMLASLRGGSSDL--S-DEDEDAEDSSANIITDLVYQGASLQAQTDRTGEMALHLAARYSRADAAKRLLDAGA
TAN-1	1860	TPPQG--EVDADCMDVNVRGPDGFTPLMIASCSGGGLETGNS-EEEEDAP---A-VISDFIYQGASLHNQTDRTGETALHLAARYSRSDAAKRLLEASA
rat NOTCH	1857	TPPQG--EVDADCMDVNVRGPDGFTPLMIASCSGGGLETGNS-EEEEDAP---A-VISDFIYQGASLHNQTDRTGETALHLAARYSRSDAAKRLLEASA
XENOPUS NOTCH	1855	TPPQG--EIEADCMDVNVRGPDGFTPLMIASCSGGGLETGNS-EEEEDA--S-ANMISDFIGQGAQLHNQTDRTGETALHLAARYARADAAKRLLESSA
DROSOPH NOTCH	1883	TPPA---HQDGGKHDVDARGPCGLTPLMIAAVRGGGLDTGEDIENNED---STAQVISDLLAQGAELNATMDKTGETSLHLAARFARADAAKRLFHAGA

CDC10-3 CDC10-4 CDC10-5 CDC10-6

hN5k		DANAQDNMGRCPLHAAVAADAQGVFQILIRNRVTDLDARMNDGTTPLILAARLAVEGMVAELINCQADVNAVDDHGKSALHWAAAVNNVEATLLLLKNGANRDMQD
TAN-1	1952	DANIQDNMGRTPLHAAVSADAQGVFQILIRNRATDLDARMHDGTTPLILAARLAVEGMLEDLINSHADVNAVDDLGKSALHWAAAVNNVDAAVVLLKNGANKDMQN
rat NOTCH	1944	DANIQDNMGRTPLHAAVSADAQGVFQILLRNRATDLDARMHDGTTPLILAARLAVEGMLEDLINSHADVNAVDDLGKSALHWAAAVNNVDAAVVLLKNGANKDMQN
XENOPUS NOTCH	1950	DANVQDNMGRTPLHAAVAADAQGVFQILIRNRATDLDARMFDGTTPLILAARLAVEGMVEELINAHADVNAVDEFGKSALHWAAAVNNVDAAAVLLKNSANKDMQN
DROSOPH NOTCH	1976	DANCQDNTGRTPLHAAVAADAMGVFQILLRNRATNLNARMHDGTTPLILAARLAIEGMVEDLITADADRNAADNSGKTALHWAAAVNNTEAVNILLMHHANRDAQD

PRIMER cdc-1

GA C/T GCI AA C/T GTI CA A/G GA C/T AA C/T ATG GG

hN5k		NKEETPLFLAAREGSYEAAKILLDHFANRDITDHMDRLPRDVARDRMHHDIVRLLDEYNVTPSPP--GTVL--TSALSPV----------ICGPNRSFLSLKHTP
TAN-1	2058	NREETPLFLAAREGSYETAKVLLDHFANRDITDHMDRLPRDIAQERMHHDIVRLLDEYNLVRSPQLHGAPLGGTPTLSPP----------LCSPNGYLGSLKPGV
rat NOTCH	2050	NKEETPLFLAAREGSYETAKVLLDHFANRDITDHMDRLPRDIAQERMHHDIVRLLDEYNLVRSPQLHGTALGGTPTLSPT----------LCSPNGYLGNLKSAT
XENOPUS NOTCH	2056	NKEETSLFLAAREGSYETAKVLLDHYANRDITDHMDRLPRDIAQERMHHDIVHLLDEYNLVKSPTLHNGPLGAT-TLSPP----------ICSPNGYMGNMKPSV
DROSOPH NOTCH	2082	DKDETPLFLAAREGSYEACKALLDNFANREITDHMDRLPRDVASERLHHDIVRLLDE-HVPRSPQMLSMTPQAMIGSPPPGQQQPQLITQPTVISAGNGGNNGNGN

TC CAT G\A TG G\A TC ICT T\G\A AT ITC IC T\G G\A TT PRIMER cdc-3

hN5k		MGKKSRRPSAKSTMPTSLPNLAKEAKDAKGSRRKKSLSEKVQLSE--SSVTLSPVDSLESPHTYVSDTTSSPM----------
TAN-1	2154	QGKKVRKPSSKGLACGS-----KEAKDLKA-RRKKSQDGKGCLLD--SSGMLSPVDSLESPHGYLSDVASPPL----------
rat NOTCH	2144	QGKKARKPSTKGLACSS-----KEAKDLKA-RRKKSQDGKGCLLD--SSSMLSPVDSLESPHGYLSDVASPPL----------
XENOPUS NOTCH	2149	QSKKARKPSIKGNGC-------KEAKELKA-RRKKSQDGKTTLLDSGSSGVLSPVDSLESTHGYLSDVSSPPL----------
DROSOPH NOTCH	2187	ASGKQSNQTAKQKAA-------KKAKLIEGS-PDNGLDATGSDRRHASSKKTSAASKKAANLNGLNPGQLTGGVSGVPGVPPTNSAAQAAAAAAAAVAAMSHELEGS

NLS BNTS CK-II cdc2 cdc2

FIG.12B

```
hN5k                 ----------------------------------------------------------------ITSPGIDQASPNPML--ATAAPPAPVHAQHALSF
TAN-1          2218  ----------------------------------------------------------------LRSPR--QQSPSVPLNHLPGMPDTHLGIGHLNVA
rat NOTCH      2209  ----------------------------------------------------------------LRSPR--QQSPSMPLSHLPGMPDTHLGISHLNVA
XENOPUS NOTCH  2214  ----------------------------------------------------------------MTSPR--QQSPSMPLNHLTSMPESQLGMNHINMA
DROSOPH NOTCH  2285  PVGVGMGGNLPSPYDTSSMYSNAMAAPLANGNPNTGAKQPRSYEDCIKNAQSMQSLQGNGLDMIKLDNYAYSMGSPR--QQELLNGQGLGMNGNGQRNGVGPGVLP
                                                                                    CK-II                CK-II

hN5k                 SNLHEMQ-------------------PLAHGASTVLPSVSQLLSHHHIVSPGS--GSAGSLSRLHPVPVPADW--MNRMEVNETQYNEMFGMVLAPAEG-THPGI
TAN-1          2250  A-KPEMAALGGGGRLAFETGPPRLSHLPVASGTSTVLGSSSGGALNFTVGGSTSLNGQCEWLSRLQSGMVPNQYNPLRGSVAPGPLSTQAPSLQHG-MVGPLHSSL
rat NOTCH      2242  A-KPEMAALAGGSRLAFEPPPPRLSHLPVASSASTVLSTNGTGAMNFTVGAPASLNGQCEWLPRLQNGMVPSQYNPLRPGVTPGTLSTQAAGLQHGMM-SPIHSSL
XENOPUS NOTCH  2247  T-KQEMAA--GSNRMAFDAMVPRLTHL-NASSPNTIMS---NGSMHFTVGGAPTMNSQCDWLARLQNGMVQNQYDPIRNGIQQGN-AQQAQALQHGLMTS-LHNGL
DROSOPH NOTCH  2390  GGLCGMGGLSGAGNGNSHEQGLSPPYS-NQSPPHSVQSSLALSPHAYLGSPSPAKSRPSLPTSPTHIQAMRHATQQKQFGGSNLNSLLGGANGGGVVGGGGGGGGV

hN5k                 APQSRPPEGK-------------HITTPREPLPP-IV-TFQLIPKGSIAQPAG----------------APQPQSTCPPAVAGPLPTMYQIP-----EMARL-P
TAN-1          2354  AASALSQMMS------------YQGLPSTRLATQPHLVQTQQVQPQNLQMQQQNLQPANIQQQQSLQPPPPPPQPHLGVSSAASGHLGRSFLSGEPSQADVQPLGP
rat NOTCH      2344  STNTLSPII-------------YQGLPNTRLATQPHLVQTQQVQPQNLQIQPQN----------LQPPS---QPHLSVSSAANGHLGRSFLSGEPSQADVQPLGP
XENOPUS NOTCH  2343  PATTLSQMMT------------YQAMPNTRLANQPHLMQAQQMQQQQN----------------LQLHQSMQQQHHN-SSTTSTHINSPFCSSDISQTDLQQM--
DROSOPH NOTCH  2495  VGQGPQNSPVSLGIISPTGSDMGIMLAPPQSSKNSAIMQTISPQQQQQQQQQQQQQHQQQQQQQQQQQQQQQQQQLGGLEFGSAGLDLNG-FCGSPDSFHSGQMNPP

hN5k                 SVAFPTAMMPQQDGQVAQTILPAYHPFPASVGKYHTPPSQHSYASSNAAERTPSHSGHLQGEHPYLTPSPESPDQWSSSSPHSA-SDWSDVTTSPTP
TAN-1          2448  SSLAVHTILPQ-ESPALPTSLPSSLVPPVTAAQFLTPPSQHSY-SS-PVENTPSHQLQVP-EHPFLTPSPESPDQWSSSSPHSNVSDWSEGVSSPPT
rat NOTCH      2423  SSLPVHTILPQ-ESQALPTSLPSSMVPPMTTTQFLTPPSQHSY-SSSPVDNTPSHQLQVP-EHPFLTPSPESPDQWSSSSRHSNISDWSEGISSPPT
XENOPUS NOTCH  2416  SSNNIHSVMPQ-DTQIFAASLPSNLTQSMTTAQFLTPPSQHSY-SS-PMDNTPSHQLQVP-DHPFLTPSPESPDQWSSSSPHSNMSDWSEGISSPPT
DROSOPH NOTCH  2599  S---IQSSMSG-SSPSTNMLSPSSQHNQQAFYQYLTPSSQHS------GGHTPQHLVQTL-D-SYPTPSPESPGHWSSSSPRSN-SDWSEGVQSPAA
```

PEST-CONTAINING REGION

FIG.12C

Potential signal cleavage site

```
hum N    MP------- ---------- ----ALRPAL LWALLALWLC CA-----APA HA-------L
TAN-1    MP------- ---------- --------PL LAPLLCLALL PA-----LAA RG-------P
Xen N    MD------- ---------- ---------- RIGLAVLLCS LP-----VLT QG-------L
Dros N   MQSQRSRRRS RAPNTWICFW INKMHAVASL PASLPLLLLT LAFANLPNIV RGTDTALVAA

hum N    MLGKATCRCA SGFTGEDCQY STSHPCFVSR PCLNGGTCHM LSRDT-YECT CQVGFTGKEC
Tan-1    GVADYACSCA LGFSGPLCLT PLDNAC-LTN PCRNGGTCDL LT-LTEYKCR CPPGWSGKSC
Xen N    NAIDFICHCP VGFTDKVCLT PVDNAC-VNN PCRNGGTCEL LNSVTEYKCR CPPGWTGDSC
Dros N   GRPGISCKCP LGFDESLCEI AVPNAC-DHV TCLNGGTCQL KT-LEEYTCA CANGYTGERC

hum N    NLPGSYQCQC PQGFTGQYCD SLYVPCAPSP CVNGGTCRQT GDFTFECNCL PGFEGSTCER
TAN-1    NEVGSYRCVC RATHTGPNCE RPYVPCSPSP CQNGGTCRPT GDVTHECACL PGFTGQNCEE
Xen N    NEFGSYRCTC QNRFTGRNCD EPYVPCNPSP CLNGGTCRQT DDTSYDCTCL PGFSGQNCEE
Dros N   NTHGSYQCMC PTGYTGKDCD TKYNPCSPSP CQNAGICRSN G-LSYECKCP KGFEGKNCEQ
```

EGF-like Repeats

```
QCRDGYEPCV NEGMCVTYHN GTGYCKCPEG FLGEYCQHRD PCE-KNRCQN GGTC--VAQA   83
RCSQPGETCL NGGKCEA-AN GTEACVCGGA FVGPRCQDPN PCL-STPCKN AGTCHVVDRR   80
RCTQTAEMCL NGGRCEMTPG GTGVCLCGNL YFGERCQFPN PCTIKNQCMN FGTCEPVLQG   90
SCTSVG--CQ NGGTCVTQLN GKTYCACDSH YVGDYCEHRN PCN-SMRCQN GGTCQVTFRN  117

QWTDACLSHP CANGSTCTTV --ANQFSCKC LTGFTGQKCE TDVNEC-DIP GHCQHGGTCL  199
QQADPCASNP CANGGQCLPF --EASYICHC PPSFHGPTCR QDVNECGQKP RLCRHGGTCH  196
QQADPCASNP CANGGKCLPF --EIQYICKC PPGFHGATCK QDINEC-S-Q NPCKNGGQCI  195
ETKNLCASSP CRNGATCTAL AGSSSFTCSC PPGFTGDTCS YDIEEC-Q-S NPCKYGGICV  233

NIDDCPNHRC QNGGVCVDGV NTYNCRCPPQ WTGQFCTEDV DECLLQPNA- CQNGGTCANR  318
NIDDCPGNNC KNGGACVDGV NTYNCPCPPE WTGQYCTEDV DECQLMPNA- CQNGGTCHNT  315
NIDDCPSNNC RNGGTCVDGV NTYNCQCPPD WTGQYCTEDV DECQLMPNA- CQNGGTCHNT  314
NYDDCLGHLC QNGGTCIDGI SDYTCRCPPN FTGRFCQDDV DECAQRDHPV CQNGATCTNT  352
```

FIG.13A

hum N	NGGYGCVCVN GWSGDDCSEN IDDCAFASCT PGSTCIDRVA SFSCMCPEGK AGLLCHLDDA	
TAN-1	HGGYNCVCVN GWTGEDCSEN IDDCASAACF HGATCHDRVA SFYCECPHGR TGLLCHLNDA	
Xen N	YGGYNCVCVN GWTGEDCSEN IDDCANAACH SGATCHDRVA SFYCECPHGR TGLLCHLDNA	
Dros N	HGSYSCICVN GWAGLDCSNN TDDCKQAACF YGATCIDGVG SFYCQCTKGK TGLLCHLDDA	
hum N	AFHCECLKGY AGPRCEMDIN ECHSDPCQND ATCLDKIGGF TCLCMPGFKG VHCELEINEC	
TAN-1	SFECQCLQGY TGPRCEIDVN ECVSNPCQND ATCLDQIGEF QCMCMPGYEG VHCEVNTDEC	
Xen N	SFQCNCPQGY AGPRCEIDVN ECLSNPCQND STCLDQIGEF QCICMPGYEG LYCETNIDEC	
Dros N	SYRCNCSQGF TGPRCETNIN ECESHPCQNE GSCLDDPGTF RCVCMPGFTG TQCEIDIDEC	
hum N	ATGFTGVLCE ENIDNCDPDP CHHGQCQDGI DSYTCICNPG YMGAICSDQI DECYSSPCLN	
TAN-1	TEGYTGTHCE VDIDECDPDP CHYGSCKDGV ATFTCLCRPG YTGHHCETNI NECSSQPCRL	
Xen N	TEGFTGRHCE QDINECIPDP CHYGTCKDGI ATFTCLCRPG YTGRLCDNDI NECLSKPCLN	
Dros N	PPGYTGTSCE ININDCDSNP CHRGKCIDDV NSFKCLCDPG YTGYICQKQI NECESNPCQF	
hum N	CISNPCHKGA LCDTNPLNGQ YICTCPQGYK GADCTEDVDE CAMANSNPCE HAGKCVNTDG	438
TAN-1	CISNPCNEGS NCDTNPVNGK AICTCPSGYT GPACSQDVDE CSLG-ANPCE HAGKCINTLG	434
Xen N	CISNPCNEGS NCDTNPVNGK AICTCPPGYT GPACNNDVDE CSLG-ANPCE HGGRCTNTLG	433
Dros N	CTSNPCHADA ICDTSPINGS YACSCATGYK GVDCSEDIDE CDQG—SPCE HNGICVNTPG	470
hum N	QSNPCVNNGQ CVDKVNRFQC LCPPGFTGPV CQIDIDDCSS TPCLNGAKCI DHPNGYECQC	558
TAN-1	ASSPCLHNGR CLDKINEFQC ECPTGFTGHL CQYDVDECAS TPCKNGAKCL DGPNTYTCVC	554
Xen N	ASNPCLHNGK CIDKINEFRC DCPTGFSGNL CQHDFDECTS TPCKNGAKCL DGPNSYTCQC	553
Dros N	QSNPCLNDGT CHDKINGFKC SCALGFTGAR CQINIDDCQS QPCRNRGICH DSIAGYSCEC	590
hum N	DGRCIDLVNG YQCNCQPGTS GVNCEINFDD CASNPCIHG- ICMDGINRYS CVCSPGFTGQ	677
TAN-1	RGTCQDPDNA YLCFCLKGTT GPNCEINLDD CASSPCDSG- TCLDKIDGYE CACEPGYTGS	673
Xen N	GGQCTDRENG YICTCPKGTT GVNCETKIDD CASNLCDNG- KCIDKIDGYE CTCEPGYTGK	672
Dros N	DGHCQDRVGS YYCQCQAGTS GKNCEVNVNE CHSNPCNNGA TCIDGINSYK CQCVPGFTGQ	710

FIG.13B

hum N	RCNIDIDECA SNPCRKGATC INGVNGFRCI CPEGPHHPSC YSQVNECLSN PCI-HGNCTG	
TAN-1	MCNSNIDECA GNPCHNGGTC EDGINGFTCR CPEGYHDPTC LSEVNECNSN PCV-HGACRD	
Xen N	LCNININECD SNPCRNGGTC KDQINGFTCV CPDGYHDHMC LSEVNECNSN PCI-HGACHD	
Dros N	HCEKNVDECI SSPCANNGVC IDQVNGYKCE CPRGFYDAHC LSDVDECASN PCVNEGRCED	
hum N	DECASNPCLN QGTCFDDISG YTCHCVLPYT GKNCQTVLAP CSPNPCENAA VCKESPNFES	
TAN-1	NECASNPCLN KGTCIDDVAG YKCNCLLPYT GATCEVVLAP CAPSPCRNGG ECRQSEDYES	
Xen N	NECSSNPCLN HGTCIDDVAG YKCNCMLPYT GAICEAVLAP CAGSPCKNGG RCKESEDFET	
Dros N	DDCVTNPCGN GGTCIDKVNG YKCVCKVPFT GRDCESKMDP CASNRCKNEA KCTPSSNFLD	
hum N	CLANPCQNGG SCMDGVNTFS CLCLPGFTGD KCQTDNMECL SEPCKNGGTC SDYVNSYTCK	
TAN-1	CRPNPCHNGG SCTDGINTAF CDCLPGFRGT FCEEDINECA SDPCRNGANC TDCVDSYTCT	
Xen N	CQPNPCHNGG SCSDGINMFF CNCPAGFRGP KCEEDINECA SNPCKNGANC TDCVNSYTCT	
Dros N	CASFPCQNGG TCLDGIGDYS CLCVDGFDGK HCETDINECL SQPCQNGATC SQYVNSYTCT	
	GLSGYKCLCD AGWVGINCEV DKNECLSNPC QNGGTCDNLV NGYRCTCKKG FKGYNCQVNI	796
	SLNGYKCDCD PGWSGTNCDI NNNECESNPC VNGGTCKDMT SGIVCTCREG FSGPNCQTNI	792
	GVNGYKCDCE AGWSGSNCDI NNNECESNPC MNGGTCKDMT GAYICTCKAG FSGPNCQTNI	791
	GINEFICHCP PGYTGKRCEL DIDECSSNPC QHGGTCYDKL NAFSCQCMPG YTGQKCETNI	830
	YTCLCA-PGW QGQRCTIDID EC-ISKPCMN HGLCHNTQGS YMCECPPGFS GMDCEEDIDD	914
	FSCVCPTAGA KGQTCEVDIN EC-VLSPCRH GASCQNTHGG YRCHCQAGYS GRNCETDIDD	911
	FSCECP-PGW QGQTCEIDMN EC-VNRPCRN GATCQNTNGS YKCNCKPGYT GRNCEMDIDD	909
	FSCTCK-LGY TGRYCDEDID ECSLSSPCRN GASCLNVPGS YRCLCTKGYE GRDCAINTDD	949
	CQAGFDGVHC ENNINECTES SCFNGGTCVD GINSFSCLCP VGFTGSFCLH EINECSSHPC	1034
	CPAGFSGIHC ENNTPDCTES SCFNGGTCVD GINSFTCLCP PGFTGSYCQH VVNECDSRPC	1031
	CQPGFSGIHC ESNTPDCTES SCFNGGTCID GINTFTCQCP PGFTGSYCQH DINECDSKPC	1029
	CPLGFSGINC QTNDEDCTES SCLNGGSCID GINGYNCSCL AGYSGANCQY KLNKCDSNPC	1069

FIG.13C

hum N	LNEGTCVDGL GTYRCSCPLG YTGKNCQTLV NLCSRSPCKN KGTCVQKKAE SQCLCPSGWA	
TAN-1	LLGGTCQDGR GLHRCTCPQG YTGPNCQNLV HWCDSSPCKN GGKCWQTHTQ YRCECPSGWT	
Xen N	LNGGTCQDSY GTYKCTCPQG YTGLNCQNLV RWCDSSPCKN GGKCWQTNNF YRCECKSGWT	
Dros N	LNGATCHEQN NEYTCHCPSG FTGKQCSEYV DWCGQSPCEN GATCSQMKHQ FSCKCSAGWT	
hum N	SNPCQHGATC SDFIGGYRCE CVPGYQGVNC EYEVDECQNQ PCQNGGTCID LVNHFKCSCP	
TAN-1	PSPCQNGATC TDYLGGYSCK CVAGYHGVNC SEEIDECLSH PCQNGGTCLD LPNTYKCSCP	
Xen N	PNPCQNGATC TDYLGGYSCE CVAGYHGVNC SEEINECLSH PCQNGGTCID LINTYKCSCP	
Dros N	SQPCQNGGTC RDLIGAYECQ CRQGFQGQNC ELNIDDCAPN PCQNGGTCHD RVMNFSCSCP	
hum N	CLSNPCSSEG SLDCIQLTND YLCVCRSAFT GRHCETFVDV CPQMPCLNGG TCAVASNMPD	
TAN-1	CLSNPCDARG TQNCVQRVND FHCECRAGHT GRRCESVING CKGKPCKNGG TCAVASNTAR	
Xen N	CLSNPCDSRG TQNCIQLVND YRCECRQGFT GRRCESVVDG CKGMPCRNGG TCAVASNTER	
Dros N	CLSNPCSNAG TLDCVQLVNN YHCNCRPGHM GRHCEHKVDF CAQSPCQNGG NCNI----RQS	
	GAYCDVPNVS CDIAASRRGV LVEHLCQHSG VCINAGNTHY CQCPLGYTGS YCEEQLDECA	1154
	GLYCDVPSVS CEVAAQRQGV DVARLCQHGG LCVDAGNTHH CRCQAGYTGS YCEDLVDECS	1151
	GVYCDVPSVS CEVAAKQQGV DIVHLCRNSG MCVDTGNTHF CRCQAGYTGS YCEEQVDECS	1149
	GKLCDVQTIS CQDAADRKGL SLRQLC-NNG TCKDYGNSHV CYCSQGYAGS YCQKEIDECQ	1188
	PGTRGLLCEE NIDDCAR---- -----GPHCLN GGQCMDRIGG YSCRCLPGFA GERCEGDINE	1267
	RGTQGVHCEI NVDDCNPPVD PVSRSPKCFN NGTCVDQVGG YSCTCPPGFV GERCEGDVNE	1271
	RGTQGVHCEI NVDDCTPFYD SFTLEPKCFN NGKCIDRVGG YNCICPPGFV GERCEGDVNE	1269
	PGTMGIICEI NKDDCKP---- -----GACHN NGSCIDRVGG FECVCQPGFV GARCEGDINE	1300
	GFICRCPPGF SGARCQS---- SCGQVKCRKG EQCVHTAS-- GPRCFCPSP- --RDCES----	1376
	GFICKCPAGF EGATCENDAR TCGSLRCLNG GTCISGPR-- SPTCLCLGPF TGPECQFPAS	1389
	GFICKCPPGF DGATCEYDSR TCSNLRCQNG GTCISVLT-- SSKCVCSEGY TGATCQYPVI	1387
	GHHCICNNGF YGKNCELSGQ DCDSNPCRVG -NCVVADEGF GYRCECPRGT LGEHCEIDTL	1415

FIG.13D

```
hum N     -GC-ASSPCQ HGGSCHPQRQ PPYYSCQCAP PFSGSRCEL- -YTAPP---- -S-----TPP
TAN-1     SPCLGGNPCY NQGTCEPTSE SPFYRCLCPA KFNGLLCHIL DYSFGG---- -GAGRDIPPP
Xen N     SPC-ASHPCY NGGTCQFFAE EPFFQCFCPK NFNGLFCHIL DYEFPG---- -GLGKNITPP
Dros N    DEC-SPNPCA QGAACEDLLG D--YECLCPS KWKGKRCDIY DANYPGWNGG SGSGNDRYAA

hum N     NN-QCDELCN TVECLFDNFE CQGNSKTCK- -YDKYCADHF KDNHCNQGCN SEECGWDGLD
TAN-1     SDGHCDSQCN SAGCLFDGFD CQRAEGQCNP LYDQYCKDHF SDGHCDQGCN SAECEWDGLD
Xen N     NDGKCDSQCN NTGCLYDGFD CQKVEVQCNP LYDQYCKDHF QDGHCDQGCN NAECEWDGLD
Dros N    KNGKCNEECN NAACHYDGHD CERKLKSCDS LFDAYCQKHY GDGFCDYGCN NAECSWDGLD

hum N     YYGEKSAAMK KQ--R----- ---------- ---MTRRSL PGEQ-----E QEVAGSKVFL
TAN-1     YYGREEELRK HPIKRAAEGW AAPDALLGQV KASLLPGGSE GGRRRRELDP MDVRGSIVYL
Xen N     YYGNEEELKK HHIKRSTDYW SDAPSAI--- -FSTMKESIL LGRHRRELDE MEVRGSIVYL
Dros N    WKDNVRVPEI EDTDFARKNK ILYTQQVHQ- ---------- ---------- ---TGIQIYL
```

LNR (Notch/Lin-12 Repeats)

```
---A---TCL SQYCADKARD GVCDEACNSH ACQWDGGDCS LTMENPWANC SSPLPCWDYI  1476
LIEE---ACE LPECQEDAGN KVCSLQCNNH ACGWDGGDCS LNFNDPWKNC TQSLQCWKYF  1501
DNDD---ICE NEQCSELADN KVCNANCNNH ACGWDGGDCS LNFNDPWKNC TQSLQCWKYF  1498
DLEQQRAMCD KRGCTEKQGN GICDSDCNTY ACNFDGNDCS LGI-NPWANC TAN-EXWNKF  1531

CAADQPEN-L AEGTLVIVVL MPPEQLLQDA R-SFLRALGT LLHTNLRIKR DSQGELMVYP  1591
CAEHVPER-L AAGTL-VVVV LMPPEQLRNS SFHFLRELSR VLHTNVVFKR DAHGQQMIFP  1619
C-ANMPEN-L AEGTLVLVVL MPPERLKNNS V-NFLRELSR VLHTNVVFKK DSKGEYKIYP  1615
CENKTQSPVL AEGAMSVVML MNVEAFREIQ A-QFLRNMSH MLRTTVRLKK DALGHDIIIN  1650

                                                              TM
EIDNRQCVQD SDHCFKNTDA AAALLASHAI QG---TLSYP LVSVVSESLT PERT-Q-LLY  1680
EIDNRQCVQA SSQCFQSATD VAAFLGALAS LGSL-NIPYK IEAVQSETVE PPPPAQ-LHF  1737
EIDNRQCYKS SSQCFNSATD VAAFLGALAS LGSLDTLSYK IEAVKSENME TPKPST-LYP  1730
EIDNRKCTEC FTHAVEAAEF LAATAAKHQL RNDFQ-IHSV RGIKNPGDED NGEPPANVKY  1745
```

FIG.13E

```
hum N     LLAVAVVIIL FIILLGVIMA KRKRK--HGS LWLPEGFTLR RDASNHKRRE PVGQDAVGLK
TAN-1     MYVAAAAFVL LFFVGCGVLL SRKRRRQHGQ LWFPEGFKV- SEASKKKRRE ELGEDSVGLK
Xen N     MLSMLVIPLL IIFVFMMVIV NKKRRREHDS FGSPTALFQK NPA-KRNGET PW-EDSVGLK
Dros N    VITGIILVII ALAFFGMVL- STQRKRAHGV TWFPEGFRAP AAVMSRRRRD PHGQEMRNLN

                                                    CDC-10/Ankyrin Repeats
hum N     PIDRRPWTQQ HLEAADIRRT PSLALTPPQA EQEVDVLDVN VRGPDGCTPL MLASLRGGSS
TAN-1     QTDHRQWTQQ HLDAADL-RM SAMAPTPPQG EVDADCMDVN VRGPDGFTPL MIASCSGGGL
Xen N     KTDPRQWTRQ HLDAADL-RI SSMAPTPPQG EIEADCMDVN VRGPDGFTPL MIASCSGGGL
Dros N    EADQRVWSQA HLDVVDV-R- AIM--TPP-A HQDGGKHDVD ARGPCGLTPL MIAAVRGGGL

hum N     ANAQDNMGRC PLHAAVAADA QGVFQILIRN RVTDLDARMN DGTTPLILAA RLAVEGMVAE
TAN-1     ANIQDNMGRT PLHAAVSADA QGVFQILIRN RATDLDARMH DGTTPLILAA RLAVEGMLED
Xen N     ANVQDNMGRT PLHAAVAADA QGVFQILIRN RATDLDARMF DGTTPLILAA RLAVEGMVEE
Dros N    ANCQDNTGRT PLHAAVAADA MGVFQILLRN RATNLNARMH DGTTPLILAA RLAIEGMVED

hum N     NLSVQVSEAN LIGTGTSEHW VDDE------ ---------G PQPKKVKAED EALLSE-EDD  1782
TAN-1     PLK-NASDGA LMDDNQNE-W GDED------ ---------- LETKKFRFEE PVVLPD-LDD  1837
Xen N     PIK-NMTDGS FMDDNQNE-W GDEET----- ---------- LENKRFRFEE QVILPELVDD  1831
Dros N    KQVAMQSQGV GQPGAH---W SDDESDMPLP KRQRSDPVSG VGLGNNGGYA SDHTMVSEYE  1861

hum N     DLSDEDEDAE DSSANIITDL VYQGASLQAQ TDRTGEMALH LAARYSRADA AKRLLDAGAD  1902
TAN-1     ETGNSEEE-E DAPA-VISDF IYQGASLHNQ TDRTGETALH LAARYSRSDA AKRLLEASAD  1954
Xen N     ETGNSEEE-E DASANMISDF IGQGAQLHNQ TDRTGETALH LAARYARADA AKRLLESSAD  1949
Dros N    DTGEDIENNE DSTAQVISDL LAQGAELNAT MDKTGETSLH LAARFARADA AKRLLDAGAD  1976

hum N     LINCQADVNA VDDHGKSALH WAAAVNNVEA TLLLLKNGAN RDMQDNKEET PLFLAAREGS  2022
TAN-1     LINSHADVNA VDDLGKSALH WAAAVNNVDA AVVLLKNGAN KDMQNNREET PLFLAAREGS  2074
Xen N     LINAHADVNA VDEFGKSALH WAAAVNNVDA AAVLLKNSAN KDMQNNKEET SLFLAAREGS  2069
Dros N    LITADADINA ADNSGKTALH WAAAVNNTEA VNILLMHHAN RDAQDDKDET PLFLAAREGS  2096
```

FIG.13F

```
hum N     YEAAKILLDH FANRDITDHM DRLPRDVARD RMHHDIVRLL DEYNVTPSPP --GTVL--TS
TAN-1     YETAKVLLDH FANRDITDHM DRLPRDIAQE RMHHDIVRLL DEYNLVRSPQ LHGAPLGGTP
Xen N     YETAKVLLDH YANRDITDHM DRLPRDIAQE RMHHDIVHLL DEYNLVKSPT LHNGPLGAT-
Dros N    YEACKALLDN FANREITDHM DRLPRDVASE RLHHDIVRLL DE-HVPRSPQ MLSMTPQAMI

                NLS                              CK II    cdc2        cdc2
hum N     GSRRKKSLSE KVQLSE--SS VTLSPVDSLE SPHTYVSDTT SSPM---------- ----------
TAN-1     A-RRKKSQDG KGCLLD--SS GMLSPVDSLE SPHGYLSDVA SPPL---------- ----------
Xen N     A-RRKKSQDG KTTLLDSGSS GVLSPVDSLE STHGYLSDVS SPPL---------- ----------
Dros N    GS-PDNGLDA TGSLRRKASS KKTSAASKKA ANLNGLNPGQ LTGGVSGVPG VPPTNSAAQA
          BNTS

hum N     ---------- ---------- ---------- ITSPGILQAS PNPML--ATA APPAPVHAQH
TAN-1     ---------- ---------- ---------- LPSPF--QQS PSVPLNHLPG MPDTHLGIGH
Xen N     ---------- ---------- ---------- MTSPF--QQS PSMPLNHLTS MPESQLGMNH
Dros N    YEDCIKNAQS MQSLQGNGLD MIKLDNYAYS MGSPF--QQE LLNGQGLGMN GNGQRNGVGP
          CK II                                    cdc2

hum N     ALSPV----- -----ICGP NRSFLSLKHT PMGKKSRRPS AKSTMPTSLP NLAKEAKDAK  2127
TAN-1     TLSPP----- -----LCSP NGYLGSLKPG VQGKKVRKPS SKGLACGS-- ---KEAKDLK  2178
TLSPP     TLSPP----- -----ICSP NGYMGNMKPS VQSKKARKPS IKGNGC---- ---KEAKELK  2170
GSPPPGQQQP QLITQPTVIS AGNGGNNGNG NASGKQSNQT AKQKAA---- ---KKAKLIE  2208

          ---------- ---------- ---------- ---------- ---------- ----------  2169
          ---------- ---------- ---------- ---------- ---------- ----------  2219
          ---------- ---------- ---------- ---------- ---------- ----------  2213
AAAAAAAVAA MSHELEGSPV GVGMGGNLPS PYDTSSMYSN AMAAPLANGN PNTGAKQPPS  2327

ALSFSNLHEM Q--------- ---------- -PLAHGASTV LPSVSQLLSH HHIVSPGS--  2235
LNVAA-KPEM AALGGGGRLA FETGPPRLSH LPVASGTSTV LGSSSGGALN FTVGGSTSLN  2306
INMAT-KQEM AA--GSNRMA FDAMVPRLTH L-NASSPNTI MS---NGSMH FTVGGAPTMN  2294
GVLPGGLCGM GGLSGAGNGN SHEQGLSPPY SNQSPPHSVQ SSLALSPHAY LGSPSPAKSR  2445
```

FIG.13G

hum N	GSAGSLSRLH PVPVPADW-- MNRMEVNETQ YNEMFGMVLA PAEG-THPGI APQSRPPEGK	
TAN-1	GQCEWLSRLQ SGMVPNQYNP LRGSVAPGPL STQAPSLQHG -MVGPLHSSL AASALSQMMS	
Xen N	SQCDWLARLQ NGMVQNQYDP IRNGIQQGN- AQQAQALQHG LMTS-LHNGL PATTLSQMMT	
Dros N	PSLPTSPTHI QAMRHATQQK QFGGSNLNSL LGGANGGGVV GGGGGGGGGV GQGPQNSPVS	
hum N	APQPQSTCPP AVAGPLPTMY QIP-----EM ARL-PSVAFP TAMMPQQDGQ VAQTILPAYH	
TAN-1	PPQPHLGVSS AASGHLGRSF LSGEPSQADV QPLGPSSLAV HTILPQ-ESP ALPTSLPSSL	
Xen N	MQQQHHN-SS TTSTHINSPF CSSDISQTDL QQM--SSNNI HSVMPQ-DTQ IFAASLPSNL	
Dros N	QQQLGGLEFG SAGLDLNG-F CGSPDSFHSG QMNPPS---I QSSMSG-SSP STNMLSPSSQ	
hum N	SDWSDVTTSP TPGGAGGGQR GPGTHMSEPPHNN MQVYA	
TAN-1	SDWSEGVSSP PT-----SMQ SQIARIPEAFK	
Xen N	SDWSEGISSP PT-----SMQ PQRTHIPEAFK	
Dros N	SDWSEGVQSP AANNLYISGG HQANKGSEAIYI	

----------	---HITTPRE PLPP-IV-TF QLIPKGSIAQ PAG------ ----------	2320
----------	-YQGLPSTRL ATQPHLVQTQ QVQPQNLQMQ QQNLQPANIQ QQQSLQPPPP	2414
----------	-YQAMPNTRL ANQPHLMQAQ QMQQQQN--- ---------- ----LQLHQS	2384
LGIISPTGSD	MGIMLAPPQS SKNSAIMQTI SPQQQQQQQQ QQQQQHQQQQ QQQQQQQQQQ	2565

PEST -containing Region

PFPASVGKYP	TPPSQHSYAS SNAAERTPSH SGHLQGEHPY LTPSPESPDQ WSSSSPHSA-	2433
VPPVTAAQFL	TPPSQHSY-S S-PVENTPSH QLQVP-EGPF LTPSPESPDQ WSSSSPHSNV	2530
TQSMTTAQFL	TPPSQHSY-S S-PMDNTPSH QLQVP-DHPF LTPSPESPDQ WSSSSPHSNM	2497
HNQQAFYQYL	TPSSQHS--- ---GGHTPQH LVQTL-D-SY PTPSPESPGH WSSSSPRSN-	2671

2471
2556
2523
2703

FIG.13H

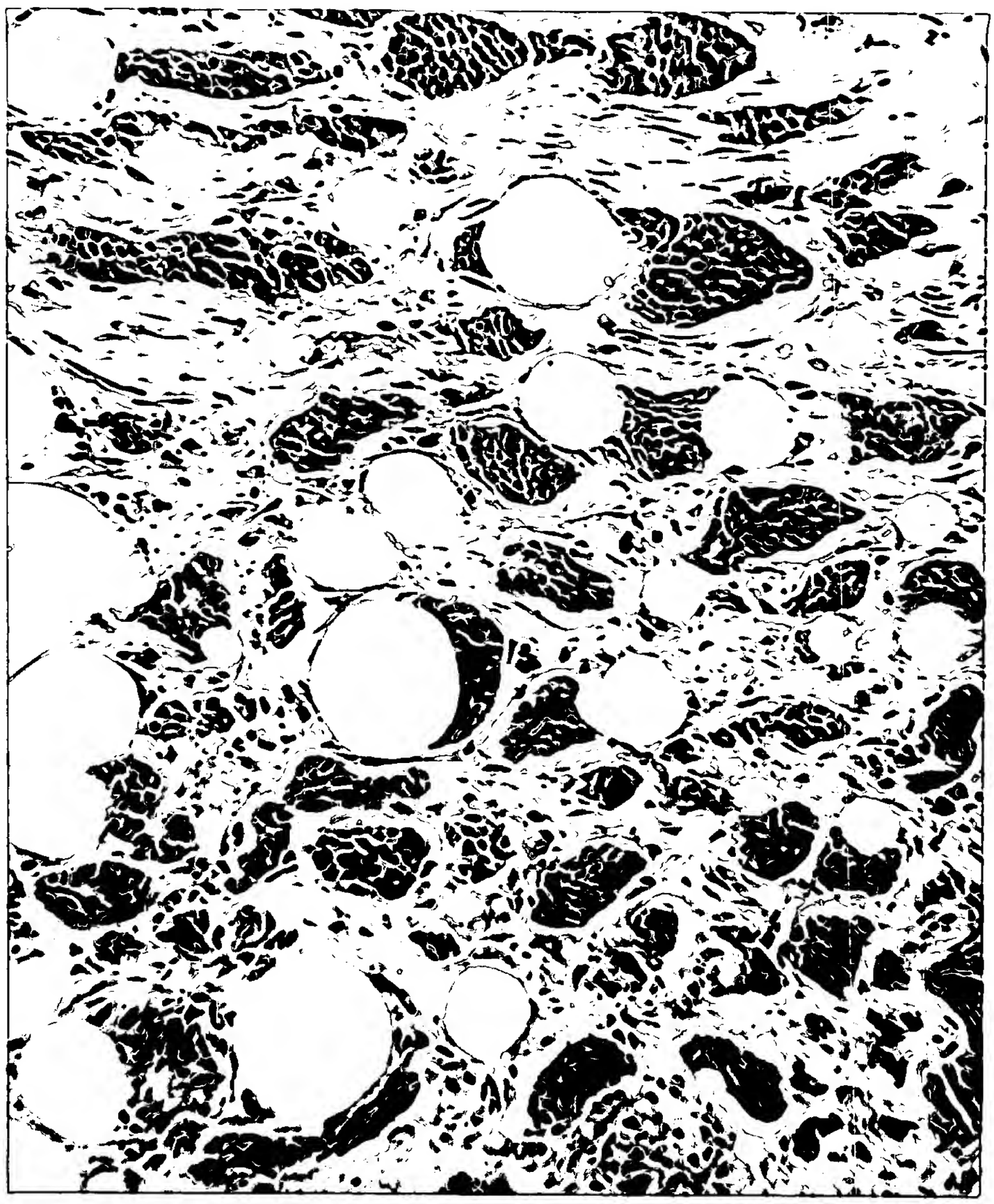


FIG. 14

FIG. 15B

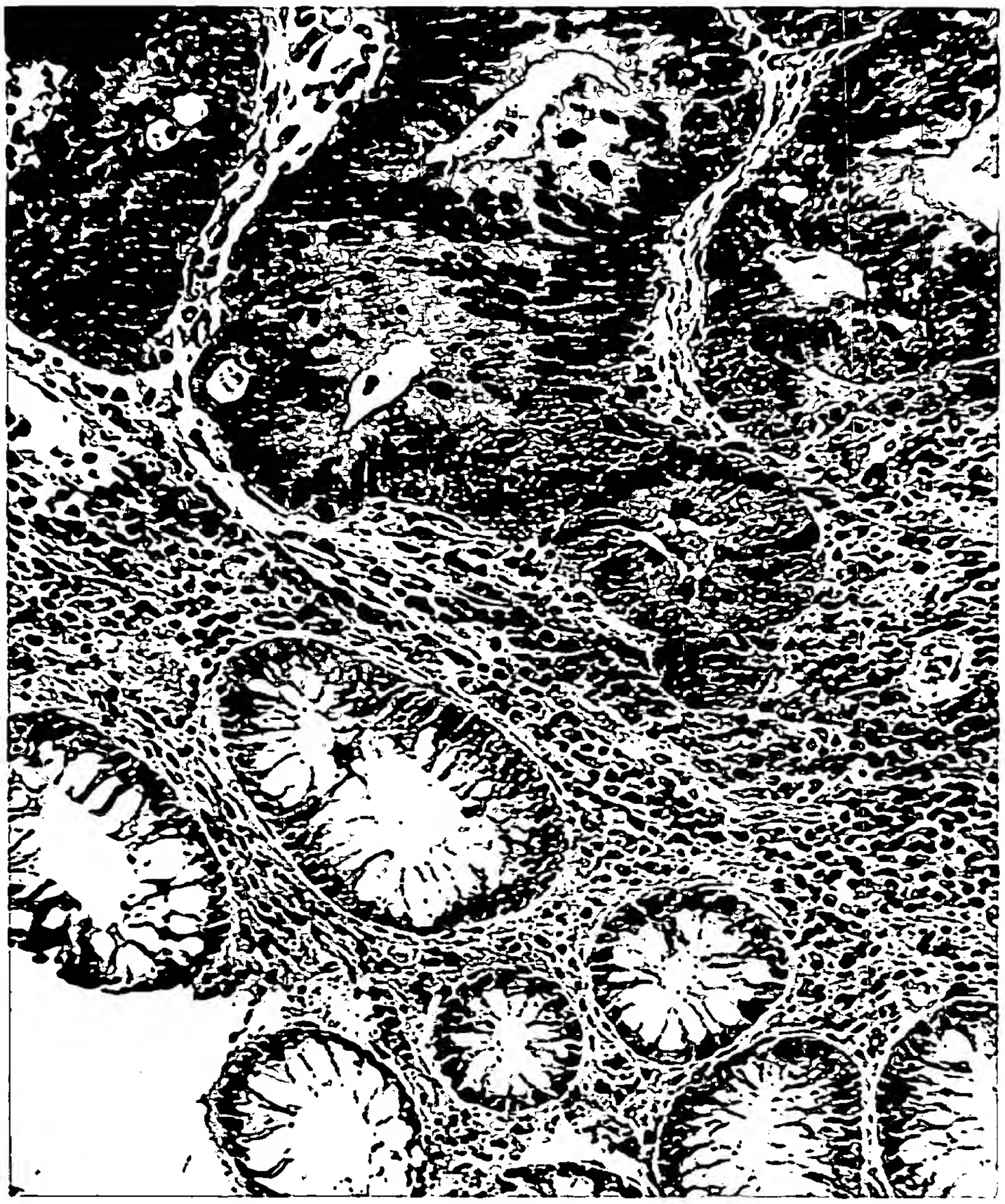
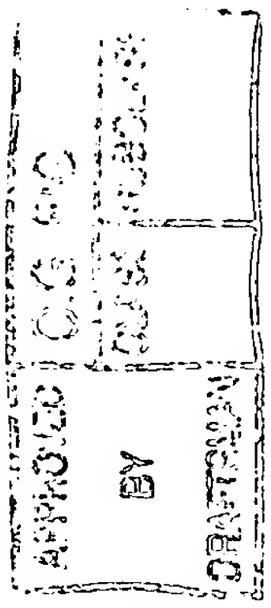


FIG. 15A

FIG. 16A



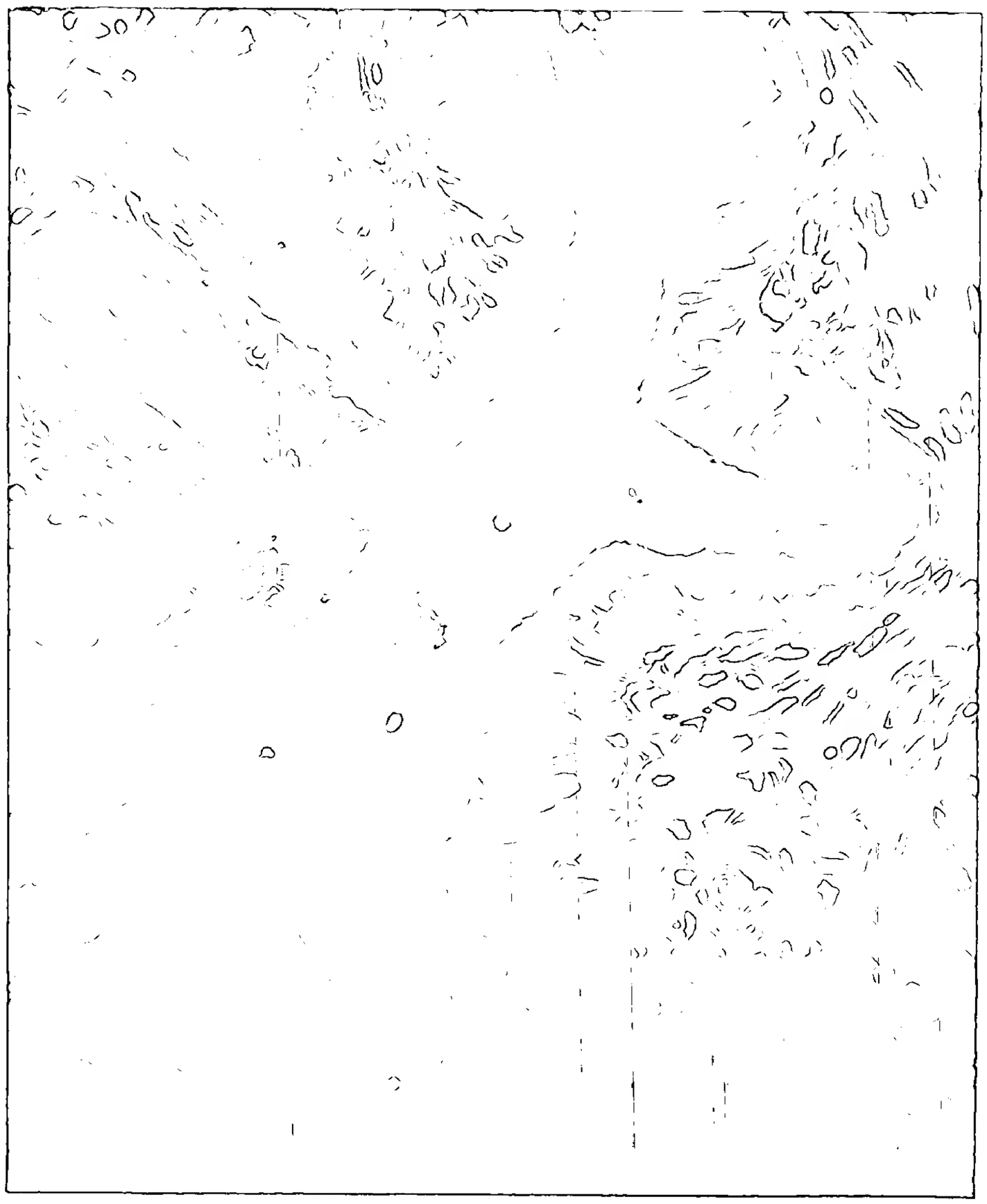


FIG. 16B

```
        10         20         30         40         50         60         70         80         90
         *          *          *          *          *          *          *          *          *
GGAATTCCGC CCGCCCTGCG CCCCGCTCTG CTGTGGGCGC TGCTGGCGCT CTGGCTGTGC TGCGCGGCCC CCGCGCATGC ATTGCAGTGT
      P  A  L  R  P  A  L  L  W  A  L  L  A  L  W  L  C  C  A  A  P  A  H  A  L  Q  C>

       100        110        120        130        140        150        160        170        180
         *          *          *          *          *          *          *          *          *
CGAGATGGCT ATGAACCCTG TGTAAATGAA GGAATGTGTG TTACCTACCA CAATGGCACA GGATACTGCA AATGTCCAGA AGGCTTCTTG
 R  D  G  Y  E  P  C  V  N  E  G  M  C  V  T  Y  H  N  G  T  G  Y  C  K  C  P  E  G  F  L>

       190        200        210        220        230        240        250        260        270
         *          *          *          *          *          *          *          *          *
GGGGAATATT GTCAACATCG AGACCCCTGT GAGAAGAACC GCTGCCAGAA TGGTGGGACT TGTGTGGCCC AGGCCATGCT GGGGAAAGCC
 G  E  Y  C  Q  H  R  D  P  C  E  K  N  R  C  Q  N  G  G  T  C  V  A  Q  A  M  L  G  K  A>

       280        290        300        310        320        330        340        350        360
         *          *          *          *          *          *          *          *          *
ACGTGCCGAT GTGCCTCAGG GTTTACAGGA GAGGACTGCC AGTACTCAAC ATCTCATCCA TGCTTTGTGT CTCGACCCTG CCTGAATGGC
 T  C  R  C  A  S  G  F  T  G  E  D  C  Q  Y  S  T  S  H  P  C  F  V  S  R  P  C  L  N  G>

       370        380        390        400        410        420        430        440        450
         *          *          *          *          *          *          *          *          *
GGCACATGCC ATATGCTCAG CCGGGATACC TATGAGTGCA CCTGTCAAGT CGGGTTTACA GGTAAGGAGT GCCAATGGAC GGATGCCTGC
 G  T  C  H  M  L  S  R  D  T  Y  E  C  T  C  Q  V  G  F  T  G  K  E  C  Q  W  T  D  A  C>

       460        470        480        490        500        510        520        530        540
         *          *          *          *          *          *          *          *          *
CTGTCTCATC CCTGTGCAAA TGGAAGTACC TGTACCACTG TGGCCAACCA GTTCTCCTGC AAATGCCTCA CAGGCTTCAC AGGGCAGAAA
 L  S  H  P  C  A  N  G  S  T  C  T  T  V  A  N  Q  F  S  C  K  C  L  T  G  F  T  G  Q  K>

       550        560        570        580        590        600        610        620        630
         *          *          *          *          *          *          *          *          *
TGTGAGACTG ATGTCAATGA GTGTGACATT CCAGGACACT GCCAGCATGG TGGCACCTGC CTCAACCTGC CTGGTTCCTA CCAGTGCCAG
 C  E  T  D  V  N  E  C  D  I  P  G  H  C  Q  H  G  G  T  C  L  N  L  P  G  S  Y  Q  C  Q>

       640        650        660        670        680        690        700        710        720
         *          *          *          *          *          *          *          *          *
TGCCCTCAGG GCTTCACAGG CCAGTACTGT GACAGCCTGT ATGTGCCCTG TGCACCCTCA CCTTGTGTCA ATGGAGGCAC CTGTCGGCAG
 C  P  Q  G  F  T  G  Q  Y  C  D  S  L  Y  V  P  C  A  P  S  P  C  V  N  G  G  T  C  R  Q>

       730        740        750        760        770        780        790        800        810
         *          *          *          *          *          *          *          *          *
ACTGGTGACT TCACTTTTGA GTGCAACTGC CTTCCAGGTT TTGAAGGGAG CACCTGTGAG AGGAATATTG ATGACTGCCC TAACCACAGG
 T  G  D  F  T  F  E  C  N  C  L  P  G  F  E  G  S  T  C  E  R  N  I  D  D  C  P  N  H  R>
```

FIG.17A

```
      820        830        840        850        860        870        880        890        900
       *          *          *          *          *          *          *          *          *
TGTCAGAATG GAGGGGTTTG TGTGGATGGG GTCAACACTT ACAACTGCCG CTGTCCCCCA CAATGGACAG GACAGTTCTG CACAGAGGAT
 C  Q  N  G  G  V  C  V  D  G  V  N  T  Y  N  C  R  C  P  P  Q  W  T  G  Q  F  C  T  E  D>

      910        920        930        940        950        960        970        980        990
       *          *          *          *          *          *          *          *          *
GTGGATGAAT GCCTGCTGCA GCCCAATGCC TGTCAAAATG GGGGCACCTG TGCCAACCGC AATGGAGGCT ATGGCTGTGT ATGTGTCAAC
 V  D  E  C  L  L  Q  P  N  A  C  Q  N  G  G  T  C  A  N  R  N  G  G  Y  G  C  V  C  V  N>

     1000       1010       1020       1030       1040       1050       1060       1070       1080
       *          *          *          *          *          *          *          *          *
GGCTGGAGTG GAGATGACTG CAGTGAGAAC ATTGATGATT GTGCCTTCGC CTCCTGTACT CCAGGCTCCA CCTGCATCGA CCGTGTGGCC
 G  W  S  G  D  D  C  S  E  N  I  D  D  C  A  F  A  S  C  T  P  G  S  T  C  I  D  R  V  A>

     1090       1100       1110       1120       1130       1140       1150       1160       1170
       *          *          *          *          *          *          *          *          *
TCCTTCTCTT GCATGTGCCC AGAGGGGAAG GCAGGTCTCC TGTGTCATCT GGATGATGCA TGCATCAGCA ATCCTTGCCA CAAGGGGGCA
 S  F  S  C  M  C  P  E  G  K  A  G  L  L  C  H  L  D  D  A  C  I  S  N  P  C  H  K  G  A>

     1180       1190       1200       1210       1220       1230       1240       1250       1260
       *          *          *          *          *          *          *          *          *
CTGTGTGACA CCAACCCCCT AAATGGGCAA TATATTTGCA CCTGCCCACA AGGCTACAAA GGGGCTGACT GCACAGAAGA TGTGGATGAA
 L  C  D  T  N  P  L  N  G  Q  Y  I  C  T  C  P  Q  G  Y  K  G  A  D  C  T  E  D  V  D  E>

     1270       1280       1290       1300       1310       1320       1330       1340       1350
       *          *          *          *          *          *          *          *          *
TGTGCCATGG CCAATAGCAA TCCTTGTGAG CATGCAGGAA AATGTGTGAA CACGGATGGC GCCTTCCACT GTGAGTGTCT GAAGGGTTAT
 C  A  M  A  N  S  N  P  C  E  H  A  G  K  C  V  N  T  D  G  A  F  H  C  E  C  L  K  G  Y>

     1360       1370       1380       1390       1400       1410       1420       1430       1440
       *          *          *          *          *          *          *          *          *
GCAGGACCTC GTTGTGAGAT GGACATCAAT GAGTGCCATT CAGACCCCTG CCAGAATGAT GCTACCTGTC TGGATAAGAT TGGAGGCTTC
 A  G  P  R  C  E  M  D  I  N  E  C  H  S  D  P  C  Q  N  D  A  T  C  L  D  K  I  G  G  F>

     1450       1460       1470       1480       1490       1500       1510       1520       1530
       *          *          *          *          *          *          *          *          *
ACATGTCTGT GCATGCCAGG TTTCAAAGGT GTGCATTGTG AATTAGAAAT AAATGAATGT CAGAGCAACC CTTGTGTGAA CAATGGGCAG
 T  C  L  C  M  P  G  F  K  G  V  H  C  E  L  E  I  N  E  C  Q  S  N  P  C  V  N  N  G  Q>

     1540       1550       1560       1570       1580       1590       1600       1610       1620
       *          *          *          *          *          *          *          *          *
TGTGTGGATA AAGTCAATCG TTTCCAGTGC CTGTGTCCTC CTGGTTTCAC TGGGCCAGTT TGCCAGATTG ATATTGATGA CTGTTCCAGT
 C  V  D  K  V  N  R  F  Q  C  L  C  P  P  G  F  T  G  P  V  C  Q  I  D  I  D  D  C  S  S>
```

FIG.17B

```
      1630       1640       1650       1660       1670       1680       1690       1700       1710
       *          *          *          *          *          *          *          *          *
ACTCCGTGTC TGAATGGGGC AAAGTGTATC GATCACCCGA ATGGCTATGA ATGCCAGTGT GCCACAGGTT TCACTGGTGT GTTGTGTGAG
 T  P  C   L  N  G  A   K  C  I   D  H  P   N  G  Y  E   C  Q  C   A  T  G   F  T  G  V   L  C  E>

      1720       1730       1740       1750       1760       1770       1780       1790       1800
       *          *          *          *          *          *          *          *          *
GAGAACATTG ACAACTGTGA CCCCGATCCT TGCCACCATG GTCAGTGTCA GGATGGTATT GATTCCTACA CCTGCATCTG CAATCCCGGC
 E  N  I   D  N  C  D   P  D  P   C  H  H   G  Q  C  Q   D  G  I   D  S  Y   T  C  I  C   N  P  G>

      1810       1820       1830       1840       1850       1860       1870       1880       1890
       *          *          *          *          *          *          *          *          *
TACATGGGCG CCATCTGCAG TGACCAGATT GATGAATGTT ACAGCAGCCC TTGCCTGAAC GATGGTCGCT GCATTGACCT GGTCAATGGC
 Y  M  G   A  I  C  S   D  Q  I   D  E  C   Y  S  S  P   C  L  N   D  G  R   C  I  D  L   V  N  G>

      1900       1910       1920       1930       1940       1950       1960       1970       1980
       *          *          *          *          *          *          *          *          *
TACCAGTGCA ACTGCCAGCC AGGCACGTCA GGGGTTAATT GTGAAATTAA TTTTGATGAC TGTGCAAGTA ACCCTTGTAT CCATGGAATC
 Y  Q  C   N  C  Q  P   G  T  S   G  V  N   C  E  I  N   F  D  D   C  A  S   N  P  C  I   H  G  I>

      1990       2000       2010       2020       2030       2040       2050       2060       2070
       *          *          *          *          *          *          *          *          *
TGTATGGATG GCATTAATCG CTACAGTTGT GTCTGCTCAC CAGGATTCAC AGGGCAGAGA TGTAACATTG ACATTGATGA GTGTGCCTCC
 C  M  D   G  I  N  R   Y  S  C   V  C  S   P  G  F  T   G  Q  R   C  N  I   D  I  D  E   C  A  S>

      2080       2090       2100       2110       2120       2130       2140       2150       2160
       *          *          *          *          *          *          *          *          *
AATCCCTGTC GCAAGGGTGC AACATGTATC AACGGTGTGA ATGGTTTCCG CTGTATATGC CCCGAGGGAC CCCATCACCC CAGCTGCTAC
 N  P  C   R  K  G  A   T  C  I   N  G  V   N  G  F  R   C  I  C   P  E  G   P  H  H  P   S  C  Y>

      2170       2180       2190       2200       2210       2220       2230       2240       2250
       *          *          *          *          *          *          *          *          *
TCACAGGTGA ACGAATGCCT GAGCAATCCC TGCATCCATG GAAACTGTAC TGGAGGTCTC AGTGGATATA AGTGTCTCTG TGATGCAGGC
 S  Q  V   N  E  C  L   S  N  P   C  I  H   G  N  C  T   G  G  L   S  G  Y   K  C  L  C   D  A  G>

      2260       2270       2280       2290       2300       2310       2320       2330       2340
       *          *          *          *          *          *          *          *          *
TGGGTTGGCA TCAACTGTGA AGTGGACAAA AATGAATGCC TTTCGAATCC ATGCCAGAAT GGAGGAACTT GTGACAATCT GGTGAATGGA
 W  V  G   I  N  C  E   V  D  K   N  E  C   L  S  N  P   C  Q  N   G  G  T   C  D  N  L   V  N  G>

      2350       2360       2370       2380       2390       2400       2410       2420       2430
       *          *          *          *          *          *          *          *          *
TACAGGTGTA CTTGCAAGAA GGGCTTTAAA GGCTATAACT GCCAGGTGAA TATTGATGAA TGTGCCTCAA ATCCATGCCT GAACCAAGGA
 Y  R  C   T  C  K  F   G  F  K   G  Y  N   C  Q  V  N   I  D  E   C  A  S   N  P  C  L   N  Q  G>
```

FIG.17C

```
      2440       2450       2460       2470       2480       2490       2500       2510       2520
       *          *          *          *          *          *          *          *          *
ACCTGCTTTG ATGACATAAG TGGCTACACT TGCCACTGTG TGCTGCCATA CACAGGCAAG AATTGTCAGA CAGTATTGGC TCCCTGTTCC
 T  C  F   D  D  I  S   G  Y  T   C  H  C   V  L  P  Y   T  G  K   N  C  Q   T  V  L  A   P  C  S>

      2530       2540       2550       2560       2570       2580       2590       2600       2610
       *          *          *          *          *          *          *          *          *
CCAAACCCTT GTGAGAATGC TGCTGTTTGC AAAGAGTCAC CAAATTTTGA GAGTTATACT TGCTTGTGTG CTCCTGGCTG GCAAGGTCAG
 P  N  P   C  E  N  A   A  V  C   K  E  S   P  N  F  E   S  Y  T   C  L  C   A  P  G  W   Q  G  Q>

      2620       2630       2640       2650       2660       2670       2680       2690       2700
       *          *          *          *          *          *          *          *          *
CGGTGTACCA TTGACATTGA CGAGTGTATC TCCAAGCCCT GCATGAACCA TGGTCTCTGC CATAACACCC AGGGCAGCTA CATGTGTGAA
 R  C  T   I  D  I  D   E  C  I   S  K  P   C  M  N  H   G  L  C   H  N  T   Q  G  S  Y   M  C  E>

      2710       2720       2730       2740       2750       2760       2770       2780       2790
       *          *          *          *          *          *          *          *          *
TGTCCACCAG GCTTCAGTGG TATGGACTGT GAGGAGGACA TTGATGACTG CCTTGCCAAT CCTTGCCAGA ATGGAGGTTC CTGTATGGAT
 C  P  P   G  F  S  G   M  D  C   E  E  D   I  D  D  C   L  A  N   P  C  Q   N  G  G  S   C  M  D>

      2800       2810       2820       2830       2840       2850       2860       2870       2880
       *          *          *          *          *          *          *          *          *
GGAGTGAATA CTTTCTCCTG CCTCTGCCTT CCGGGTTTCA CTGGGGATAA GTGCCAGACA GACATGAATG AGTGTCTGAG TGAACCCTGT
 G  V  N   T  F  S  C   L  C  L   P  G  F   T  G  D  K   C  Q  T   D  M  N   E  C  L  S   E  P  C>

      2890       2900       2910       2920       2930       2940       2950       2960       2970
       *          *          *          *          *          *          *          *          *
AAGAATGGAG GGACCTGCTC TGACTACGTC AACAGTTACA CTTGCAAGTG CCAGGCAGGA TTTGATGGAG TCCATTGTGA GAACAACATC
 K  N  G   G  T  C  S   D  Y  V   N  S  Y   T  C  K  C   Q  A  G   F  D  G   V  H  C  E   N  N  I>

      2980       2990       3000       3010       3020       3030       3040       3050       3060
       *          *          *          *          *          *          *          *          *
AATGAGTGCA CTGAGAGCTC CTGTTTCAAT GGTGGCACAT GTGTTGATGG GATTAACTCC TTCTCTTGCT TGTGCCCTGT GGGTTTCACT
 N  E  C   T  E  S  S   C  F  N   G  G  T   C  V  D  G   I  N  S   F  S  C   L  C  P  V   G  F  T>

      3070       3080       3090       3100       3110       3120       3130       3140       3150
       *          *          *          *          *          *          *          *          *
GGATCCTTCT GCCTCCATGA GATCAATGAA TGCAGCTCTC ATCCATGCCT GAATGAGGGA ACGTGTGTTG ATGGCCTGGG TACCTACCGC
 G  S  F   C  L  H  E   I  N  E   C  S  S   H  P  C  L   N  E  G   T  C  V   D  G  L  G   T  Y  R>

      3160       3170       3180       3190       3200       3210       3220       3230       3240
       *          *          *          *          *          *          *          *          *
TGCAGCTGCC CCCTGGGCTA CACTGGGAAA AACTGTCAGA CCCTGGTGAA TCTCTGCAGT CGGTCTCCAT GTAAAAACAA AGGTACTTGT
 C  S  C   P  L  G  Y   T  G  K   N  C  Q   T  L  V  N   L  C  S   R  S  P   C  K  N  K   G  T  C>
```

FIG.17D

```
      3250       3260       3270       3280       3290       3300       3310       3320       3330
       *          *          *          *          *          *          *          *          *
GTTCAGAAAA AAGCAGAGTC CCAGTGCCTA TGTCCATCTG GATGGGCTGG TGCCTATTGT GACGTGCCCA ATGTCTCTTG TGACATAGCA
 V  Q  K   K  A  E  S   Q  C  L   C  P  S   G  W  A  G   A  Y  C   D  V  P   N  V  S  C   D  I  A>

      3340       3350       3360       3370       3380       3390       3400       3410       3420
       *          *          *          *          *          *          *          *          *
GCCTCCAGGA GAGGTGTGCT TGTTGAACAC TTGTGCCAGC ACTCAGGTGT CTGCATCAAT GCTGGCAACA CGCATTACTG TCAGTGCCCC
 A  S  R   R  G  V  L   V  E  H   L  C  Q   H  S  G  V   C  I  N   A  G  N   T  H  Y  C   Q  C  P>

      3430       3440       3450       3460       3470       3480       3490       3500       3510
       *          *          *          *          *          *          *          *          *
CTGGGCTATA CTGGGAGCTA CTGTGAGGAG CAACTCGATG AGTGTGCGTC CAACCCCTGC CAGCACGGGG CAACATGCAG TGACTTCATT
 L  G  Y   T  G  S  Y   C  E  E   Q  L  D   E  C  A  S   N  P  C   Q  H  G   A  T  C  S   D  F  I>

      3520       3530       3540       3550       3560       3570       3580       3590       3600
       *          *          *          *          *          *          *          *          *
GGTGGATACA GATGCGAGTG TGTCCCAGGC TATCAGGGTG TCAACTGTGA GTATGAAGTG GATGAGTGCC AGAATCAGCC CTGCCAGAAT
 G  G  Y   R  C  E  C   V  P  G   Y  Q  G   V  N  C  E   Y  E  V   D  E  C   Q  N  Q  P   C  Q  N>

      3610       3620       3630       3640       3650       3660       3670       3680       3690
       *          *          *          *          *          *          *          *          *
GGAGGCACCT GTATTGACCT TGTGAACCAT TTCAAGTGCT CTTGCCCACC AGGCACTCGG GGCCTACTCT GTGAAGAGAA CATTGATGAC
 G  G  T   C  I  D  L   V  N  H   F  K  C   S  C  P  P   G  T  R   G  L  L   C  E  E  N   I  D  D>

      3700       3710       3720       3730       3740       3750       3760       3770       3780
       *          *          *          *          *          *          *          *          *
TGTGCCCGGG GTCCCCATTG CCTTAATGGT GGTCAGTGCA TGGATAGGAT TGGAGGCTAC AGTTGTCGCT GCTTGCCTGG CTTTGCTGGG
 C  A  R   G  P  H  C   L  N  G   G  Q  C   M  D  R  I   G  G  Y   S  C  R   C  L  P  G   F  A  G>

      3790       3800       3810       3820       3830       3840       3850       3860       3870
       *          *          *          *          *          *          *          *          *
GAGCGTTGTG AGGGAGACAT CAACGAGTGC CTCTCCAACC CCTGCAGCTC TGAGGGCAGC CTGGACTGTA TACAGCTCAC CAATGACTAC
 E  R  C   E  G  D  I   N  E  C   L  S  N   P  C  S  S   E  G  S   L  D  C   I  Q  L  T   N  D  Y>

      3880       3890       3900       3910       3920       3930       3940       3950       3960
       *          *          *          *          *          *          *          *          *
CTGTGTGTTT GCCGTAGTGC CTTTACTGGC CGGCACTGTG AAACCTTCGT CGATGTGTGT CCCCAGATGC CCTGCCTGAA TGGAGGGACT
 L  C  V   C  R  S  A   F  T  G   R  H  C   E  T  F  V   D  V  C   P  Q  M   P  C  L  N   G  G  T>

      3970       3980       3990       4000       4010       4020       4030       4040       4050
       *          *          *          *          *          *          *          *          *
TGTGCTGTGG CCAGTAACAT GCCTGATGGT TTCATTTGCC GTTGTCCCCC GGGATTTTCC GGGGCAAGGT GCCAGAGCAG CTGTGGACAA
 C  A  V   A  S  N  M   P  D  G   F  I  C   R  C  P  P   G  F  S   G  A  R   C  Q  S  S   C  G  Q>
```

FIG.17E

```
      4060       4070       4080       4090       4100       4110       4120       4130       4140
       *          *          *          *          *          *          *          *          *
GTGAAATGTA GGAAGGGGGA GCAGTGTGTG CACACCGCCT CTGGACCCCG CTGCTTCTGC CCCAGTCCCC GGGACTGCGA GTCAGGCTGT
 V  K  C   R  K  G  E   Q  C  V   H  T  A   S  G  P  R   C  F  C   P  S  P   R  D  C  E   S  G  C>

      4150       4160       4170       4180       4190       4200       4210       4220       4230
       *          *          *          *          *          *          *          *          *
GCCAGTAGCC CCTGCCAGCA CGGGGGCAGC TGCCACCCTC AGCGCCAGCC TCCTTATTAC TCCTGCCAGT GTGCCCCACC ATTCTCGGGT
 A  S  S   P  C  Q  H   G  G  S   C  H  P   Q  R  Q  P   P  Y  Y   S  C  Q   C  A  P  P   F  S  G>

      4240       4250       4260       4270       4280       4290       4300       4310       4320
       *          *          *          *          *          *          *          *          *
AGCCGCTGTG AACTCTACAC GGCACCCCCC AGCACCCCTC CTGCCACCTG TCTGAGCCAG TATTGTGCCG ACAAAGCTCG GGATGGCGTC
 S  R  C   E  L  Y  T   A  P  P   S  T  P   P  A  T  C   L  S  Q   Y  C  A   D  K  A  R   D  G  V>

      4330       4340       4350       4360       4370       4380       4390       4400       4410
       *          *          *          *          *          *          *          *          *
TGTGATGAGG CCTGCAACAG CCATGCCTGC CAGTGGGATG GGGGTGACTG TTCTCTCACC ATGGAGAACC CCTGGGCCAA CTGCTCCTCC
 C  D  E   A  C  N  S   H  A  C   Q  W  D   G  G  D  C   S  L  T   M  E  N   P  W  A  N   C  S  S>

      4420       4430       4440       4450       4460       4470       4480       4490       4500
       *          *          *          *          *          *          *          *          *
CCACTTCCCT GCTGGGATTA TATCAACAAC CAGTGTGATG AGCTGTGCAA CACGGTCGAG TGCCTGTTTG ACAACTTTGA ATGCCAGGGG
 P  L  P   C  W  D  Y   I  N  N   Q  C  D   E  L  C  N   T  V  E   C  L  F   D  N  F  E   C  Q  G>

      4510       4520       4530       4540       4550       4560       4570       4580       4590
       *          *          *          *          *          *          *          *          *
AACAGCAAGA CATGCAAGTA TGACAAATAC TGTGCAGACC ACTTCAAAGA CAACCACTGT AACCAGGGGT GCAACAGTGA GGAGTGTGGT
 N  S  K   T  C  K  Y   D  K  Y   C  A  D   H  F  K  D   N  H  C   N  Q  G   C  N  S  E   E  C  G>

      4600       4610       4620       4630       4640       4650       4660       4670       4680
       *          *          *          *          *          *          *          *          *
TGGGATGGGC TGGACTGTGC TGCTGACCAA CCTGAGAACC TGGCAGAAGG TACCCTGGTT ATTGTGGTAT TGATGCCACC TGAACAACTG
 W  D  G   L  D  C  A   A  D  Q   P  E  N   L  A  E  G   T  L  V   I  V  V   L  M  P  P   E  Q  L>

      4690       4700       4710       4720       4730       4740       4750       4760       4770
       *          *          *          *          *          *          *          *          *
CTCCAGGATG CTCGCAGCTT CTTGCGGGCA CTGGGTACCC TGCTCCACAC CAACCTGCGC ATTAAGCGGG ACTCCCAGGG GGAACTCATG
 L  Q  D   A  R  S  F   L  R  A   L  G  T   L  L  H  T   N  L  R   I  K  R   D  S  Q  G   E  L  M>

      4780       4790       4800       4810       4820       4830       4840       4850       4860
       *          *          *          *          *          *          *          *          *
GTGTACCCCT ATTATGGTGA GAAGTCAGCT GCTATGAAGA AACAGAGGAT GACACGCAGA TCCCTTCCTG GTGAACAAGA ACAGGAGGTG
 V  Y  P   Y  Y  G  E   K  S  A   A  M  K   K  Q  R  M   T  R  R   S  L  P   G  E  Q  E   Q  E  V>
```

FIG.17F

```
      4870       4880       4890       4900       4910       4920       4930       4940       4950
       *          *          *          *          *          *          *          *          *
GCTGGCTCTA AAGTCTTTCT GGAAATTGAC AACCGCCAGT GTGTTCAAGA CTCAGACCAC TGCTTCAAGA ACACGGATGC AGCAGCAGCT
 A  G  S    K  V  F  L    E  I  D    N  R  Q    C  V  Q  D    S  D  H    C  F  K    N  T  D  A    A  A  A>

      4960       4970       4980       4990       5000       5010       5020       5030       5040
       *          *          *          *          *          *          *          *          *
CTCCTGGCCT CTCACGCCAT ACAGGGGACC CTGTCATACC CTCTTGTGTC TGTCGTCAGT GAATCCCTGA CTCCAGAACG CACTCAGCTC
 L  L  A    S  H  A  I    Q  G  T    L  S  Y    P  L  V  S    V  V  S    E  S  L    T  P  E  R    T  Q  L>

      5050       5060       5070       5080       5090       5100       5110       5120       5130
       *          *          *          *          *          *          *          *          *
CTCTATCTCC TTGCTGTTGC TGTTGTCATC ATTCTGTTTA TTATTCTGCT GGGGGTAATC ATGGCAAAAC GAAAGCGTAA GCATGGCTCT
 L  Y  L    L  A  V  A    V  V  I    I  L  F    I  I  L  L    G  V  I    M  A  K  R    K  R  K  H    G  S>

      5140       5150       5160       5170       5180       5190       5200       5210       5220
       *          *          *          *          *          *          *          *          *
CTCTGGCTGC CTGAAGGTTT CACTCTTCGC CGAGATGCAA GCAATCACAA GCGTCGTGAG CCAGTGGGAC AGGATGCTGT GGGGCTGAAA
 L  W  L    P  E  G  F    T  L  R    R  D  A    S  N  H  K    R  R  E    P  V  G    Q  D  A  V    G  L  K>

      5230       5240       5250       5260       5270       5280       5290       5300       5310
       *          *          *          *          *          *          *          *          *
AATCTCTCAG TGCAAGTCTC AGAAGCTAAC CTAATTGGTA CTGGAACAAG TGAACACTGG GTCGATGATG AAGGGCCCCA GCCAAAGAAA
 N  L  S    V  Q  V  S    E  A  N    L  I  G    T  G  T  S    E  H  W    V  D  D    E  G  P  Q    P  K  K>

      5320       5330       5340       5350       5360       5370       5380       5390       5400
       *          *          *          *          *          *          *          *          *
GTAAAGGCTG AAGATGAGGC CTTACTCTCA GAAGAAGATG ACCCCATTGA TCGACGGCCA TGGACACAGC AGCACCTTGA AGCTGCAGAC
 V  K  A    E  D  E  A    L  L  S    E  E  D    D  P  I  D    R  R  P    W  T  Q    Q  H  L  E    A  A  D>

      5410       5420       5430       5440       5450       5460       5470       5480       5490
       *          *          *          *          *          *          *          *          *
ATCCGTAGGA CACCATCGCT GGCTCTCACC CCTCCTCAGG CAGAGCAGGA GGTGGATGTG TTAGATGTGA ATGTCCGTGG CCCAGATGGC
 I  R  R    T  P  S  L    A  L  T    P  P  Q    A  E  Q  E    V  D  V    L  D  V    N  V  R  G    P  D  G>

      5500       5510       5520       5530       5540       5550       5560       5570       5580
       *          *          *          *          *          *          *          *          *
TGCACCCCAT TGATGTTGGC TTCTCTCCGA GGAGGCAGCT CAGATTTGAG TGATGAAGAT GAAGATGCAG AGGACTCTTC TGCTAACATC
 C  T  P    L  M  L  A    S  L  R    G  G  S    S  D  L  S    D  E  D    E  D  A    E  D  S  S    A  N  I>

      5590       5600       5610       5620       5630       5640       5650       5660       5670
       *          *          *          *          *          *          *          *          *
ATCACAGACT TGGTCTACCA GGGTGCCAGC CTCCAGGCCC AGACAGACCG GACTGGTGAG ATGGCCCTGC ACCTTGCAGC CCGCTACTCA
 I  T  D    L  V  Y  Q    G  A  S    L  Q  A    Q  T  D  R    T  G  E    M  A  L    H  L  A  A    R  Y  S>
```

FIG.17G

```
      5680       5690       5700       5710       5720       5730       5740       5750       5760
       *          *          *          *          *          *          *          *          *
CCGGCTGATG CTGCCAAGCG TCTCCTGGAT GCAGGTGCAG ATGCCAATGC CCAGGACAAC ATGGGCCGCT GTCCACTCCA TGCTGCAGTG
 R  A  D    A  A  K  R    L  L  D    A  G  A    D  A  N  A    Q  D  N    M  G  R    C  P  L  H    A  A  V>

      5770       5780       5790       5800       5810       5820       5830       5840       5850
       *          *          *          *          *          *          *          *          *
GCAGCTGATG CCCAAGGTGT CTTCCAGATT CTGATTCGCA ACCGAGTAAC TGATCTAGAT GCCAGGATGA ATGATGGTAC TACACCCCTG
 A  A  D    A  Q  G  V    F  Q  I    L  I  R    N  R  V  T    D  L  D    A  R  M    N  D  G  T    T  P  L>

      5860       5870       5880       5890       5900       5910       5920       5930       5940
       *          *          *          *          *          *          *          *          *
ATCCTGGCTG CCCGCCTGGC TGTGGAGGGA ATGGTGGCAG AACTGATCAA CTGCCAAGCG GATGTGAATG CAGTGGATGA CCATGGAAAA
 I  L  A    A  R  L  A    V  E  G    M  V  A    E  L  I  N    C  Q  A    D  V  N    A  V  D  D    H  G  K>

      5950       5960       5970       5980       5990       6000       6010       6020       6030
       *          *          *          *          *          *          *          *          *
TCTGCTCTTC ACTGGGCAGC TGCTGTCAAT AATGTGGAGG CAACTCTTTT GTTGTTGAAA AATGGGGCCA ACCGAGACAT GCAGGACAAC
 S  A  L    H  W  A  A    A  V  N    N  V  E    A  T  L  L    L  L  K    N  G  A    N  R  D  M    Q  D  N>

      6040       6050       6060       6070       6080       6090       6100       6110       6120
       *          *          *          *          *          *          *          *          *
AAGGAAGAGA CACCTCTGTT TCTTGCTGCC CGGGAGGGGA GCTATGAAGC AGCCAAGATC CTGTTAGACC ATTTTGCCAA TCGAGACATC
 K  E  E    T  P  L  F    L  A  A    R  E  G    S  Y  E  A    A  K  I    L  L  D    H  F  A  N    R  D  I>

      6130       6140       6150       6160       6170       6180       6190       6200       6210
       *          *          *          *          *          *          *          *          *
ACAGACCATA TGGATCGTCT TCCCCGGGAT GTGGCTCGGG ATCGCATGCA CCATGACATT GTGCGCCTTC TGGATGAATA CAATGTGACC
 T  D  H    M  D  R  L    P  R  D    V  A  R    D  R  M  H    H  D  I    V  R  L    L  D  E  Y    N  V  T>

      6220       6230       6240       6250       6260       6270       6280       6290       6300
       *          *          *          *          *          *          *          *          *
CCAAGCCCTC CAGGCACCGT GTTGACTTCT GCTCTCTCAC CTGTCATCTG TGGGCCCAAC AGATCTTTCC TCAGCCTGAA GCACACCCCA
 P  S  P    P  G  T  V    L  T  S    A  L  S    P  V  I  C    G  P  N    R  S  F    L  S  L  K    H  T  P>

      6310       6320       6340       6350       6360       6370       6380       6390       6400
       *          *          *          *          *          *          *          *          *
ATGGGCAAGA AGTCTAGACG GCCCAGTGCC AAGAGTACCA TGCCTACTAG CCTCCCTAAC CTTGCCAAGG AGGCAAAGGA TGCCAAGGGT
 M  G  K    K  S  R  R    P  S  A    K  S  T    M  P  T  S    L  P  N    L  A  K    E  A  K  D    A  K  G>

      6400       6410       6420       6430       6440       6450       6460       6470       6480
       *          *          *          *          *          *          *          *          *
AGTAGGAGGA AGAAGTCTCT GAGTGAGAAG GTCCAACTGT CTGAGAGTTC AGTAACTTTA TCCCCTGTTG ATTCCCTAGA ATCTCCTCAC
 S  R  R    K  K  S  L    S  E  K    V  Q  L    S  E  S  S    V  T  L    S  P  V    D  S  L  E    S  P  H>
```

FIG.17H

```
      6490        6500        6510        6520        6530        6540        6550        6560        6570
       *           *           *           *           *           *           *           *           *
ACGTATGTTT CCGACACCAC ATCCTCTCCA ATGATTACAT CCCCTGGGAT CTTACAGGCC TCACCCAACC CTATGTTGGC CACTGCCGCC
 T Y V  S D T T  S S P  M I T  S P G  I L Q  A S P  N P M  L A  T A A>

      6580        6590        6600        6610        6620        6630        6640        6650        6660
       *           *           *           *           *           *           *           *           *
CCTCCTGCCC CAGTCCATGC CCAGCATGCA CTATCTTTTT CTAACCTTCA TGAAATGCAG CCTTTGGCAC ATGGGGCCAG CACTGTGCTT
 P P A  P V H  A Q H  A L S  F S N  L H E  M Q P  L A H  G A S  T V L>

      6670        6680        6690        6700        6710        6720        6730        6740        6750
       *           *           *           *           *           *           *           *           *
CCCTCAGTGA GCCAGTTGCT ATCCCACCAC CACATTGTGT CTCCAGGCAG TGGCAGTGCT GGAAGCTTGA GTAGGCTCCA TCCAGTCCCA
 P S V  S Q L L  S H H  H I V  S P G  S G S  A G S  L S R  L H P  V P>

      6760        6770        6780        6790        6800        6810        6820        6830        6840
       *           *           *           *           *           *           *           *           *
GTCCCAGCAG ATTGGATGAA CCGCATGGAG GTGAATGAGA CCCAGTACAA TGAGATGTTT GGTATGGTCC TGGCTCCAGC TGAGGGCACC
 V P A  D W M  N R M  E V N  E T Q  Y N E  M F G  M V L  A P A  E G T>

      6850        6860        6870        6880        6890        6900        6910        6920        6930
       *           *           *           *           *           *           *           *           *
CATCCTGGCA TAGCTCCCCA GAGCAGGCCA CCTGAAGGGA AGCACATAAC CACCCCTCGG GAGCCCTTGC CCCCCATTGT GACTTTCCAG
 H P G  I A P  Q S R  P P E  G K H  I T T  P R E  P L P  P I V  T F Q>

      6940        6950        6960        6970        6980        6990        7000        7010        7020
       *           *           *           *           *           *           *           *           *
CTCATCCCTA AAGGCAGTAT TGCCCAACCA GCGGGGGCTC CCCAGCCTCA GTCCACCTGC CCTCCAGCTG TTGCGGGCCC CCTGCCCACC
 L I P  K G S  I A Q  P A G  A P Q  P Q S  T C P  P A V  A G P  L P T>

      7030        7040        7050        7060        7070        7080        7090        7100        7110
       *           *           *           *           *           *           *           *           *
ATGTACCAGA TTCCAGAAAT GGCCCGTTTG CCCAGTGTGG CTTTCCCCAC TGCCATGATG CCCCAGCAGG ACGGGCAGGT AGCTCAGACC
 M Y Q  I P E  M A R  L P S  V A F  P T A  M M P  Q Q D  G Q V  A Q T>

      7120        7130        7140        7150        7160        7170        7180        7190        7200
       *           *           *           *           *           *           *           *           *
ATTCTCCCAG CCTATCATCC TTTCCCAGCC TCTGTGGGCA AGTACCCCAC ACCCCCTTCA CAGCACAGTT ATGCTTCCTC AAATGCTGCT
 I L P  A Y H  P F P  A S V  G K Y  P T P  P S Q  H S Y  A S S  N A A>

      7210        7220        7230        7240        7250        7260        7270        7280        7290
       *           *           *           *           *           *           *           *           *
GAGCGAACAC CCAGTCACAG TGGTCACCTC CAGGGTGAGC ATCCCTACCT GACACCATCC CCAGAGTCTC CTGACCAGTG GTCAAGTTCA
 E R T  P S H  S G H  L Q G  E H P  Y L T  P S P  E S P  D Q W  S S S>
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FIG.17I

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      7300       7310       7320       7330       7340       7350       7360       7370       7380
       *          *          *          *          *          *          *          *          *
TCACCCCACT CTGCTTCTGA CTGGTCAGAT GTGACCACCA GCCCTACCCC TGGGGGTGCT GGAGGAGGTC AGCGGGGACC TGGGACACAC
 S  P  H   S  A  S  D   W  S  D   V  T  T   S  P  T  P   G  G  A   G  G  G   Q  R  G  P   G  T  H>

      7390       7400       7410       7420       7430       7440       7450       7460       7470
       *          *          *          *          *          *          *          *          *
ATGTCTGAGC CACCACACAA CAACATGCAG GTTTATGCGT GAGAGAGTCC ACCTCCAGTG TAGAGACATA ACTGACTTTT GTAAATGCTG
 M  S  E   P  P  H  N   N  M  Q   V  Y  A>

      7480       7490       7500       7510       7520       7530       7540       7550       7560
       *          *          *          *          *          *          *          *          *
CTGAGGAACA AATGAAGGTC ATCCGGGAGA GAAATGAAGA AATCTCTGGA GCCAGCTTCT AGAGGTAGGA AAGAGAAGAT GTTCTTATTC

      7570       7580       7590       7600       7610       7620       7630       7640       7650
       *          *          *          *          *          *          *          *          *
AGATAATGCA AGAGAAGCAA TTCGTCAGTT TCACTGGGTA TCTGCAAGGC TTATTGATTA TTCTAATCTA ATAAGACAAG TTTGTGGAAA

      7660       7670       7680       7690       7700       7710       7720       7730       7740
       *          *          *          *          *          *          *          *          *
TGCAAGATGA ATACAAGCCT TGGGTCCATG TTTACTCTCT TCTATTTGGA GAATAAGATG GATGCTTATT GAAGCCCAGA CATTCTTGCA

      7750       7760       7770       7780       7790       7800       7810       7820       7830
       *          *          *          *          *          *          *          *          *
GCTTGGACTG CATTTTAAGC CCTGCAGGCT TCTGCCATAT CCATGAGAAG ATTCTACACT AGCGTCCTGT TGGGAATTAT GCCCTGGAAT

      7840       7850       7860       7870       7880       7890       7900       7910       7920
       *          *          *          *          *          *          *          *          *
TCTGCCTGAA TTGACCTACG CATCTCCTCC TCCTTGGACA TTCTTTTGTC TTCATTTGGT GCTTTTGGTT TTGCACCTCT CCGTGATTGT

      7930       7940       7950       7960       7970       7980       7990       8000       8010
       *          *          *          *          *          *          *          *          *
AGCCCTACCA GCATGTTATA GGGCAAGACC TTTGTGCTTT TGATCATTCT GGCCCATGAA AGCAACTTTG GTCTCCTTTC CCCTCCTGTC

      8020       8030       8040       8050       8060       8070       8080       8090       8100
       *          *          *          *          *          *          *          *          *
TTCCCGGTAT CCCTTGGAGT CTCACAAGGT TTACTTTGGT ATGGTTCTCA GCACAAACCT TTCAAGTATG TTGTTTCTTT GGAAAATGGA

      8110       8120       8130       8140       8150       8160       8170       8180       8190
       *          *          *          *          *          *          *          *          *
CATACTGTAT TGTGTTCTCC TGCATATATC ATTCCTGGAG AGAGAAGGGG AGAAGAATAC TTTTCTTCAA CAAATTTTGG GGGCAGGAGA

      8200       8210       8220       8230       8240       8250       8260       8270       8280
       *          *          *          *          *          *          *          *          *
TCCCTTCAAG AGGCTGCACC TTAATTTTTC TTGTCTGTGT GCAGGTCTTC ATATAAACTT TACCAGGAAG AAGGGTGTGA GTTTGTTGTT
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FIG.17J

8290 8300 8310 8320 8330 8340 8350 8360 8370

TTTCTGTGTA TGGGCCTGGT CAGTGTAAAG TTTTATCCTT GATAGTCTAG TTACTATGAC CCTCCCCACT TTTTTAAAAC CAGAAAAAGG

8380 8390 8400 8410 8420 8430 8440 8450 8460

TTTGGAATGT TGGAATGACC AAGAGACAAG TTAACTCGTG CAAGAGCCAG TTACCCACCC ACAGGTCCCC CTACTTCCTG CCAAGCATTC

8470 8480 8490 8500 8510 8520 8530 8540 8550

CATTGACTGC CTGTATGGAA CACATTTGTC CCAGATCTGA GCATTCTAGG CCTGTTTCAC TCACTCACCC AGCATATGAA ACTAGTCTTA

8560 8570 8580 8590 8600 8610 8620 8630 8640

ACTGTTGAGC CTTTCCTTTC ATATCCACAG AAGACACTGT CTCAAATGTT GTACCCTTGC CATTTAGGAC TGAACTTTCC TTAGCCCAAG

8650 8660 8670 8680 8690 8700 8710 8720 8730

GGACCCAGTG ACAGTTGTCT TCCGTTTGTC AGATGATCAG TCTCTACTGA TTATCTTGCT GCTTAAAGGC CTGCTCACCA ATCTTTCTTT

8740 8750 8760 8770 8780 8790 8800 8810 8820

CACACCGTGT GGTCCGTGTT ACTGGTATAC CCAGTATGTT CTCACTGAAG ACATGGACTT TATATGTTCA AGTGCAGGAA TTGGAAAGTT

8830 8840 8850 8860 8870 8880 8890 8900 8910

GGACTTGTTT TCTATGATCC AAAACAGCCC TATAAGAAGG TTGGAAAAGG AGGAACTATA TAGCAGCCTT TGCTATTTTC TGCTACCATT

8920 8930 8940 8950 8960 8970 8980 8990 9000

TCTTTTCCTC TGAAGCGGCC ATGACATTCC CTTTGGCAAC TAACGTAGAA ACTCAACAGA ACATTTTCCT TTCCTAGAGT CACCTTTTAG

9010 9020 9030 9040 9050 9060 9070 9080 9090

ATGATAATGG ACAACTATAG ACTTGCTCAT TGTTCAGACT GATTGCCCCT CACCTGAATC CACTCTCTGT ATTCATGCTC TTGGCAATTT

9100 9110 9120 9130 9140 9150 9160 9170 9180

CTTTGACTTT CTTTTAAGGG CAGAAGCATT TTAGTTAATT GTAGATAAAG AATAGTTTTC TTCCTCTTCT CCTTGGGCCA GTTAATAATT

9190 9200 9210 9220 9230 9240 9250 9260 9270

GGTCCATGGC TACACTGCAA CTTCCGTCCA GTGCTGTGAT GCCCATGACA CCTGCAAAAT AAGTTCTGCC TGGGCATTTT GTAGATATTA

FIG.17K

9280	9290	9300	9310	9320	9330	9340	9350	9360
*	*	*	*	*	*	*	*	*
ACAGGTGAAT	TCCCGACTCT	TTTGGTTTGA	ATGACAGTTC	TCATTCCTTC	TATGGCTGCA	AGTATGCATC	AGTGCTTCCC	ACTTACCTGA
9370	9380	9390	9400	9410	9420	9430	9440	9450
*	*	*	*	*	*	*	*	*
TTTGTCTGTC	GGTGGCCCCA	TATGGAAACC	CTGCGTGTCT	GTTGGCATAA	TAGTTTACAA	ATGGTTTTTT	CAGTCCTATC	CAAATTTATT
9460	9470	9480	9490	9500	9510	9520	9530	9540
*	*	*	*	*	*	*	*	*
GAACCAACAA	AAATAATTAC	TTCTGCCCTG	AGATAAGCAG	ATTAAGTTTG	TTCATTCTCT	GCTTTATTCT	CTCCATGTGG	CAACATTCTG
9550	9560	9570	9580	9590	9600	9610	9620	9630
*	*	*	*	*	*	*	*	*
TCAGCCTCTT	TCATAGTGTG	CAAACATTTT	ATCATTCTAA	ATGGTGACTC	TCTGCCCTTG	GACCCATTTA	TTATTCACAG	ATGGGGAGAA
9640	9650	9660	9670	9680	9690	9700	9710	9720
*	*	*	*	*	*	*	*	*
CCTATCTGCA	TGGACCCTCA	CCATCCTCTG	TGCAGCACAC	ACAGTGCAGG	GAGCCAGTGG	CGATGGCGAT	GACTTTCTTC	CCCTGGGAAT

TCC

FIG.17L